RENZ LAW, LLC.

September 12, 2022

Donald Trump**,** Senator Ron Johnson, Senator Rand Paul, Rep. Jim Jordan, and others were right. As early as late April or early May of 2020 former President Trump spoke of the creation of SARS-COV2 in a lab in Wuhan, China. Since that time both the investigation and the cover-up have continued but the evidence provided herein clearly demonstrate that SARS-COV2 was indeed created in a lab in Wuhan China by EcoHealth Alliance and with funding from Anthony Fauci's NIH/NIAID.

Evidence included herein demonstrate the following key points (amongst others):

1. SARS-COV2 was created in the lab in Wuhan, China;
2. Anthony Fauci funded the creation of SARS-COV2 and lied to Congress about funding Gain-of-Function work;
3. The US Intelligence Community was aware of and appeared to have been involved with the funding of said Gain-of-Function work;
4. A number of well-connected public and private partners were involved in the Gain-of-Function work that resulted in the creation and release of SARS-COV2;
5. Anthony Fauci and others coordinated to cover-up the funding of the Gain-of-Function work that resulted in SARS-COV2.

Given the recent high-profile criminal enforcement actions taken by Congress and the DoJ, we expect immediate investigations will see bi-partisan support in light of this newly compiled information. Renz Law and Make Americans Free Again (MAFA) will provide any and all support possible in such investigations and prosecutions. Further, with the additional high-profile revelations that certain segments of the government have promoted censoring this information, presumably as part of this same cover-up, we will voluntarily support any good-faith efforts by the media to correct the record.

As has been the case since early in the pandemic, Renz Law and MAFA will continue to seek truth and justice in this matter for all that have been impacted by the worst man-made pandemic in human history.

Sincerely,

Thomas Renz

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RENZ LAW, LLC.

Answering Crucial Questions About Sars-CoV-2

Thomas Renz, attorney at law
Pamela A. Popper, Make Americans Free Again

Executive Summary

In early 2020, billions of people were told by governments and health agencies all over the world that a "novel virus" had caused severe illness in several individuals in Wuhan, China. Shortly after this announcement, people were told that the lethality rate for this virus, SARS-CoV-2, could be ten times higher than typical flu. The entire world started organizing to prevent the healthcare system from being overwhelmed with seriously ill patients, and to prevent as many deaths as possible. Government and health officials issued orders requiring businesses, schools, and houses of worship to close. People were told not to leave their homes except to purchase food and essential items and for emergency healthcare. Masks were required in all public indoor and outdoor places. Parks and beaches and trails were closed. Special events worldwide were cancelled for almost two years. Life as we know it came to a screeching halt and has not yet returned to normal.

In spite of these draconian measures, the World Health Organization reports that as of September 9, 2022, there have been over 600 million cases of SARS-CoV-2 and over 6.4 million deaths reported worldwide.[1]

Damage due to SARS-CoV-2 is not limited to illness and death from the virus itself. Hundreds of thousands of businesses were bankrupted and families lost their livelihoods. The unemployment rate skyrocketed. The incidence of depression, anxiety, and other psychological disorders increased dramatically. Unprecedented harm was inflicted on children; school closures, masks, and relentless fear resulted in developmental delays and academic failure for millions of kids of all ages.

The response to this disaster must be to prevent this from happening again. The only way to protect the world from another devastating debacle like this is to get to the bottom of its origin. Almost three years after the first SARS-CoV-2 patients were reported in Wuhan, China, most Americans still do not know the truth about the origin of SARS-CoV-2. There are many as-yet unanswered questions:

- Where did SARS-CoV-2 come from? Lab? Animal?
- If SARS-CoV-2 was developed in a lab, which one(s)?
- Who was involved in the development of SARS-CoV-2?

[1] WHO Coronavirus (COVID-19) Dashboard. https://covid19.who.int/ accessed 9.9.2022

- Who paid for it?
- And why has this information not been made public?

This document is designed to answer these questions, with the best evidence available at this time. Arriving at a conclusion required the analysis of large amounts of research, some of which is quite complex. We have done our best to summarize complex data in relatively easy-to-understand terms.

The story of SARS-CoV-2 involves many government officials and agencies; academic research centers and research centers; and funding sources. We will discuss many of them here, but have determined that only a few bare most of the responsibility for SARS-CoV-2, and this document focuses on these individuals and organizations:

- Peter Daszak and his organization EcoHealth Alliance,
- Anthony Fauci, head of The National Institute of Allergy and Infectious Diseases,
- Shi Zhengli, Chinese virologist who headed the Center for Emerging Infectious Diseases at the Wuhan Institute of Virology,
- Ralph Baric, Professor in the Department of Epidemiology and the Department of Microbiology and Immunology at the University of North Carolina, Chapel Hill.

We believe that in the coming weeks and months, partly in response to making this document public, more evidence will become available. We do not expect new disclosures to change any conclusions herein; but rather that more people coming forward will strengthen our findings.

As for how to organize our findings, we decided to relate the information as sequentially as possible, and to provide background information where appropriate. This document, is, essentially, the "story of SARS-CoV-2."

Table of Acronyms

BLAST	Basic Local Alignment Search Tool
BSL	Bio-Safety Level
CCP	Chinese Communist Party
CDC	Centers for Disease Control
DARPA	U.S. Defense Advanced Research Projects Agency
DHHS	Department of Health and Human Services
EUA	Emergency Use Authorization
FCS	Furin Cleavage Site
FOIA	Freedom of Information Act
GoF	Gain of Function
NCBI	National Center for Biotechnology Information
NIAH	National Institute of Aging
NIAID	National Institute of Allergy and Infectious Diseases
NIH	National Institutes of Health
PRC	People's Republic of China
UNCH	University of North Carolina, Chapel Hill
USAID	U.S. Agency for International Development
USG	US Government
WHO	World Health Organization
WIV	Wuhan Institute of Virology

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About Andrew G. Huff PhD.

Andrew G. Huff worked at EcoHealth Alliance for a period of time and was a first-hand witness to the design and engineering of SARS-CoV-2. Dr. Huff has provided considerable valuable information to Renz Law concerning the origin of SARS-CoV-2 and the misbehavior that took place during the planning and execution of research supported by or conducted by EcoHealth Alliance. Information from his first-hand account, which is supported by a deposition under penalty of perjury, is included in this document.

Dr. Huff served in the U.S. Army, was involved in the Global War on Terrorism in Central America, and was engaged served in combat operations in Iraq.

After returning home from Iraq, Dr. Huff completed a bachelor's degree in psychology at the University of Minnesota, one of the top psychology research institutions in the world. He worked for the U.S. Department of Veterans Affairs, both relocating and building new outpatient mental healthcare offices.

Dr. Huff then earned a master's degree in Security Technologies with a Geographic Information Systems minor, also from the University of Minnesota. He was offered a full scholarship and earned a Ph.D. in the fields of bioterrorism, biowarfare, chemical warfare, pandemics, and emerging infectious disease. His research was published in peer-reviewed journals before he submitted his dissertation for review.

Dr. Huff then worked as a Research Fellow at the Department of Homeland Security Center of Excellence. During his tenure there, he presented research at high-level government meetings and to executives in the private sector.

While employed with Sandia National Laboratories, Dr. Huff was given Department of Energy "Q" clearance ,which is equivalent to a Department of Defense "Top Secret" Clearance with a Special Access Programs designation. He analyzed national security problems, served as a subject matter expert in public health and food protection, and worked on projects related to pandemic preparedness, mitigation, and response.

When he decided to leave public sector work, he applied for a position at EcoHealth Alliance in September 2014. Dr. Peter Daszak offered, and Dr. Huff accepted, a position as Senior Scientist

in charge of the Data and Technology team. During his time at EcoHealth, Dr. Huff was prepared reports for U.S. intelligence agencies, and reviewed proposals for funding gain of function research to the National Institute for Allergies and Infectious Diseases as routine scientific tasks. He eventually was promoted to Vice President after demonstrating that he could raise funds from wealthy donors and government project sponsors; design and successfully execute sophisticated research and development projects; and build high-functioning cohesive teams rapidly.

Dr. Huff has personal knowledge and documents related to the origin of COVID-19 and has shared both with Renz Law. His personal declaration is included in this document as evidence to support many assertions we make.

What is Gain-of Function Research?

For purposes of this discussion, gain-of-function research involves manipulating viruses in a laboratory setting to investigate their potential to infect humans.

Here is a description of how gain-of-function research was conducted on a virus to make it transmissible to humans and to potentially make it more deadly to humans (in other words, the creation of SARS-CoV-2):

- First, the genome of an existing virus is mapped.
- In one approach, a virus is passaged in host animals (for example from mouse-to-mouse or ferret-to-ferret) repeatedly until a virus with different properties emerges. The virus may not have the capability of infecting a targeted animal species at the beginning of the project but gains this capability to infect the target animal through serial transmission.
- Another approach involves directly engineering changes in the genome of the virus. In the case of SARS-CoV-2, a genetically engineered spike protein created in the lab, was inserted into the genetic sequence of a virus. The high affinity of this spike protein to the ACE2 receptor in the body increased the infectivity of what became SARS-CoV-2.
- The new virus was then tested on humanized mice (biologically modified with a human receptor that enabled the new SARS-CoV-2 to enter their cells) and on human lung cells in the lab.
- Researchers succeeded in infecting human epithelial cell preparations and making the living mice sick with SARS-CoV-2. They knew they had created a virus that could infect humans.
- They then made the absurd claim that this process can happen in nature, which is why more funding should be allocated to conduct more of this type of research.

This type of research is controversial due to the risk of accidental release of a mutated virus that results from these experiments. While hundreds of researchers have spoken out against it, Dr. Anthony Fauci (head of the National Institute of Allergy and Infectious Diseases or NIAID) has historically defended this type of research. In an editorial in the *Washington Post* on December 30 2011, Fauci wrote: "[D]etermining the molecular Achilles' heel of these viruses can allow scientists to identify novel antiviral drug targets that could be used to prevent infection in those at risk or to better treat those who become infected. Decades of experience tells us that disseminating information gained through biomedical research to legitimate scientists and health

officials provides a critical foundation for generating appropriate countermeasures and, ultimately, protecting the public health."[2]

Despite Fauci's enthusiasm for it, the National Institutes of Health issued a moratorium on funding for gain-of-function research in 2014. Researchers involved in this type of work were urged to discontinue their activities until risks and benefits could be more clearly defined.[3] The October 17, 2014, document that announced the moratorium included these statements expressing concern about this type of research:

> "Gain-of-function studies, or research that improves the ability of a pathogen to cause disease, help define the fundamental nature of human-pathogen interactions, thereby enabling assessment of the pandemic potential of emerging infectious agents, informing public health and preparedness efforts, and furthering medical countermeasure development. Gain-of-function studies may entail biosafety and biosecurity risks; therefore, the risks and benefits of gain-of function research must be evaluated, both in the context of recent U.S. biosafety incidents and to keep pace with new technological developments, in order to determine which types of studies should go forward and under what conditions."
>
> "In light of recent concerns regarding biosafety and biosecurity, effective immediately, the U.S. Government (USG) will pause new USG funding for gain-of-function research on influenza, MERS or SARS viruses, as defined below. This research funding pause will be effective until a robust and broad deliberative process is completed that results in the adoption of a new USG gain-of-function research policy 1. Restrictions on new funding will apply as follows:"
>
> > "New USG funding will not be released for gain-of-function research projects that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route. The research funding pause would not apply to characterization or testing of naturally occurring influenza, MERS, and SARS viruses, unless the tests are reasonably anticipated to increase transmissibility and/or pathogenicity."

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[2] Anthony S. Fauci, Gary J. Nabel and Francis S. Collins. A flu virus risk worth taking. *Washington Post* December 30 2011 https://www.washingtonpost.com/opinions/a-flu-virus-risk-worth-taking/2011/12/30/gIQAM9sNRP_story.html accessed 9.10.2022

[3] Akst J. "Moratorium on Gain-of-Function Research." *The Scientist* October 21 2014

> "In parallel, we will encourage the currently-funded USG and non-USG funded research community to join in adopting a voluntary pause on research that meets the stated definition."[4]

It is important to note that the moratorium applied to NEW rather than existing funding. Research funded in part by The National Institute of Allergy and Infectious Diseases through EcoHealth which we have termed "The SARS-CoV-2 Creation Project" was already underway at the time the moratorium was declared. Ralph Baric, who was conducting gain of function research conducted at the University of North Carolina Chapel Hill and in partnership with researchers from the Wuhan Institute of Virology petitioned the NIH biosecurity board for an exemption from the pause. It was subsequently granted.

What is a Chimeric Virus?

A chimera, or chimeric virus, is a virus that contains genetic material from two or more distinct viruses. Chimeric viruses have been considered as potential bioweapons due to the increased lethality that can result from combining two pathogens in a lab.[5] [6] [7]

[4] U.S. Government Gain-of-Function Deliberative Process and Research Funding Pause on Selected Gain-of-Function Research Involving Influenza, MERS and SARS Viruses. https://www.phe.gov/s3/dualuse/documents/gain-of-function.pdf accessed 9.10.2022

[5] Collett Marc. "Impact of Synthetic Genomics on the Threat of Bioterrorism with Viral Agents". *Working Papers for Synthetic Genomics: Risks and Benefits for Science and Society* 2006:83–103.

[6] Smithson A. "A Bio Nightmare." *Bulletin of the Atomic Scientists* 1999 Jul: https://journals.sagepub.com/doi/full/10.2968/055004019 accessed 9.9.2022

[7] Ainscough MJ. *Next Generation Bioweapons: Genetic Engineering and BW.* US Airforce Counterproliferation Center Future Warfare Series No. 14 https://media.defense.gov/2019/Apr/11/2002115480/-1/-1/0/14NEXTGENBIOWEAPONS.PDF accessed 9.9.2022

The Wuhan Institute of Virology (WIV)

The Wuhan Institute of Virology (WIV) was originally founded in 1956 as the Wuhan Microbiology Laboratory. The Institute has operated under the jurisdiction of the Chinese Academy of Sciences since 1978. The Institute's labs range from Biosafety Level II (BSL-2) to Biosafety Level IV (BSL-4). BSL-4 labs are used for research with dangerous agents and substances.

The WIV BSL-4 LAB, which is of interest in the COVID-19 debacle, was developed by the People's Republic of China (PRC) in partnership with France following the 2003 SARS pandemic. Almost immediately after the project was undertaken, French officials expressed discomfort because it was suspected that the PRC had an ongoing biological warfare program, and the BSL-4 lab might be used for the purpose of developing biological weapons. To mitigate this concern, the parties agreed that all PRC/French research projects would be conducted under the supervision of French researchers on site at the lab. This did not, however, resolve the issue.

Disagreements between the parties continued. The French obtained information that led them to think that the PRC intended to build several BSL-4 labs. There were ongoing disputes over construction. After the Wuhan BSL-4 lab opened, the French became alarmed when the PRC requested biohazard suits that offered protection beyond what would have been necessary based on the research that should have been going on in the lab.

Of concern to everyone is the influence the Chinese Communist Party (CCP) had and continues to have on the Institute. High-level CCP officials serve on committees that decide the projects that will be undertaken in the lab and are also appointed to management positions.

Accidents at the lab have been another concern. For example, during a one-month period in 2004, the PRC reported nine new cases of SARS related to an accident during research using both live and inactivated samples of SARS-CoV.[8]

[8] The Origins of the COVID-19 Global Pandemic, Including the Roles of the Chinese Communist Party and the World Health Organization. House Foreign Affairs Committee Minority Staff Interim Report. June 12. 2020 https://gop-foreignaffairs.house.gov/wp-content/uploads/2020/08/Interim-Minority-Report-on-the-Origins-of-the-COVID-19-Global-Pandemic-Including-the-Roles-of-the-CCP-and-WHO-8.17.20.pdf accessed 9.10.2022

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The Institute is headed by Dr. Shi Zheng-Li, who is known as China's "Bat Woman" because she has spent a significant portion of her career collecting and studying bat viruses, ostensibly to facilitate the development of effective vaccines.[9] Her colleagues include scientists and physicians who have close ties to both the political and military leadership of the PRC. An example is Guo Deyin, who has conducted research on AIDS and hepatitis vaccines, as well as genetic recombination methods.

[9] Jane Qiu "How China's 'Bat Woman' Hunted Down Viruses from SARS to the New Coronavirus." *Scientific American* June 1 2020 https://www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus1/ accessed 9.10.2022

Dr. Shi's Research at WIV

In a 2010 paper, Shi and her colleagues reported the results of their research on angiotensin-converting enzyme II (ACE2) protein, which is a known SARS-CoV receptor. The group looked at ACE2 molecules from seven bat species and tested the interaction of the ACE2 receptor with the human SARS-CoV spike protein. They used HIV-based pseudo type and live SARS-CoV infection assays. Spike proteins are structures that allow coronaviruses to bind to the receptor sites on human cells.

The researchers found that the ACE2s of two bat species – *Myotis daubentoni* and *Rhinolophus sinicus* were susceptible to SARS-CoV and might be candidates as the natural host of the SARS-CoV progenitor viruses.[10]

Shi was also a member of the Chinese research team that was involved in the controversial gain-of-function research financed by the National Institute of Allergy and Infectious Diseases (headed by Anthony Fauci), The National Institute of Aging of the US National Institutes of Health, and EcoHealth Alliance (headed by Peter Daszak), and conducted in partnership with a research team (led by Ralph Baric) at the University of North Carolina Chapel Hill. In a paper published in 2015 in *Nature Medicine,* the group characterized a chimeric virus with the spike protein SHC014 that was able to use multiple genes of the SARS receptor human angiotensin-converting enzyme II (ACE2) and "replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-Cov." In other words, this virus could infect humans and quickly replicate. The article specifically stated, "…we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both *in vitro* and *in vivo*."

Furthermore, the team also reported replication of the chimeric virus in the lungs of mice. Most important, therapies typically used to treat SARS patients were found to be ineffective for treating the chimeric virus and vaccines did not prevent "infection with CoVs using the novel spike protein."[11]

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[10] Hou Y, Peng C, Yu M et al. "Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SATS-CoV entry." *Arch Virol* 2010 Oct;155(10):1563-1569
[11] Menachery VD, Yount BL, Debbink K et al. "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence." *Nat Med* 2015 Nov;21:1508-1513

Shi also conducted research on a virus called "WIV1" with clones of spike proteins and then tested the creation in humanized mice. The viruses quickly replicated, and the mice showed signs of severe pathogenesis. A peer-reviewed article reporting the results of this research listed Peter Daszak as an author.[12] What made this work especially risky was that WIV1 was already known to be potentially dangerous to humans. Baric had made this clear in an article titled "SARS-Like WIV1-CoV Poised for Human Emergence."[13]

The bottom line: Researchers at the Wuhan lab, in partnership with U.S. scientists and funded by the government (directly through the NIAH and NIAID and indirectly via grants to EcoHealth Alliance) were conducting research on bat viruses, admitted that they were successful on at least one occasion in developing one that could infect humans, and this virus seemed to be resistant to treatment and prevention with vaccines.

[12] Zeng LP, Gao YT, Ge XY et al. "Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response." *J Virol* 2016 Jun;90(14):6573-6582

[13] Menachery VD, Yount BL, Sims AC et al. "SARS-like W1V10CoV poised for human emergence." *PNAS* 2016 Mar;113(11):3048-3053

The Government and the Scientific Community Already Knew
That Gain of Function Research was a Problem

In 2012, Dutch scientist Ron Fouchier conducted gain-of-function experiments designed to make a highly lethal avian influenza virus, H5N1, more transmissible. After several attempts, the team was successful. Live ferrets were used and H5N1 acquired mutations resulting from serial passage in ferrets. The result: H5N1 was transmissible between mammals without requiring recombination in an intermediate host. And it was created in a lab.[14]

Government officials were alarmed, which led to the 2014 moratorium. Then-President Obama mandated that gain-of-function research involving influenza, SARS, and MERS be paused until a new regulatory framework could be developed. Ralph Baric, who was at the time conducting gain-of-function research in partnership with Shi Zhengli (from the Wuhan Institute), petitioned the NIH biosecurity board for an exemption from the pause. It was subsequently granted.

Meanwhile Shi's lab was unencumbered by any restrictions and gain-of-function research continued at the Wuhan Institute. She and her colleagues researched how spike proteins in both natural and chimeric SARS-like viruses bind to the ACE2 receptors in the cells of humans, bats, and animals.[15]

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[14] Herfst S, Schrauwen EJA, Linster M et al. "Airborne Transmission of Influenza A/H5N1 Virus Between Ferrets." *Science* 2012 Jun;336(6088):1534-1541
[15] Ren W, Qu X, Wendong L et al. "Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin." *J Virol* 2008 Feb;82(4):1899-1907

Government and Health Officials Were Also Aware That Labs in China Were Not Secure

In 2004, the World Health Organization voiced concerns about lab security, particularly Chinese labs. According to the WHO, a SARS outbreak in 2003 infected nine people, one of whom died. This was the third outbreak of SARS that had been traced to a lab, and the WHO indicated that a better containment policy might be necessary, as well as a reduction in the number of labs that handled SARS viruses.[16]

The Wuhan Lab was the first in China to achieve the highest level of international bioresearch containment (BSL-4), but it was well-known that security was lax. Two years before the SARS-CoV-2 debacle, U.S. Embassy officials visited the Wuhan Institute several times and sent two "Sensitive but unclassified" cables to Washington stating that safety in the lab was inadequate. One of them warned about the lab's experiments on bat viruses and the potential for human transmission and the risk of a SARS pandemic.[17]

[16] Parry J. "Breaches of safety regulations are probable cause of recent SARS outbreak, WHO says." *BMJ* 2004 May;328(7450):1222

[17] Josh Rogin. Opinion: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses. *Washington Post* April 14 2020 https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/ accessed 9.10.2022

EcoHealth Alliance and Peter Daszak

EcoHealth Alliance, formerly Wildlife Trust, is a nonprofit organization that at one time focused on wildlife conservation and matters like habitat loss, pollution, and environmental issues. In 2010, the organization rebranded itself to focus on "global health," and the "relationships between ecosystems and animal and human health."[18]

EcoHealth Alliance currently lists many partners on its website. These include[19]:

- The Centers for Disease Control
- The National Institutes of Health
- UC Davis California
- University of Pittsburgh Public Health
- Columbia University
- Princeton University
- Johns Hopkins Bloomberg School of Public Health
- Johnson and Johnson

Many of these organizations have been very involved with and some have profited from the SARS-CoV-2 debacle. For example, Johnson and Johnson is the maker of one of the COVID-19 vaccines approved under the Emergency Use Authorization, and sales have totaled billions of dollars.[20]

During a several-year period of time starting in 2008, EcoHealth Alliance received funding from two U.S. government sources specifically related to Gain of Function Research:

The U.S. Agency for International Development (USAID) through a 5-year program called PREDICT.

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[18] Entering its Fifth Decade, Wildlife Trust Re-Brands as EcoHealth Alliance. September 21 2020 https://www.ecohealthalliance.org/2010/09/entering-its-fifth-decade-wildlife-trust-re-brands-as-ecohealth-alliance

[19] https://www.ecohealthalliance.org/partners

[20] Spencer Kimball. J&J expects more than $3 billion in COVID vaccine sales this year in mixed quarterly report. *CNBC* Jan 25 2022

National Institutes of Health and National Institute of Allergy and Infectious Diseases gave grants related to "Understanding the Risk of Bat Coronavirus Emergence."[21]

Here are just a few of the grant awards:

2008 NIH/NIAID Project number 1R01AI079231-01[22]
Risk of Viral Emergence from Bats
$534,989

2009 NIH/NIAID Project number 5R01AI079231-02[23]
Risk of Viral Emergence From Bats
$535,156

2010 NIH/NIAID Project number 5R01AI0799231-03[24]
Risk of Viral Emergence From Bats
$480,423

2011 NIH/NIAID Project number 5R01AI0179231-04[25]
Risk of Viral Emergence From Bats
$510,005

2012 NIH/NIAID Project Number 5R01AI0179231-05[26]
Risk of Viral Emergence From Bats
$518,980

For the period 2002 through 2021, EcoHealth Alliance received a total of $16,874,314 in grant money from NIH/NIAID.[27] Millions of dollars were allocated for researching bat viruses but

[21] https://www.usaspending.gov/award/ASST_NON_R01AI110964_7529
[22] https://reporter.nih.gov/search/CzU6U_tz2EG7c2LWkYMjLA/project-details/7509184
[23] https://reporter.nih.gov/search/CzU6U_tz2EG7c2LWkYMjLA/project-details/7688507 accessed 9.11.2022
[24] https://reporter.nih.gov/search/CzU6U_tz2EG7c2LWkYMjLA/project-details/7934526 accessed 9.11.2022
[25] https://reporter.nih.gov/search/CzU6U_tz2EG7c2LWkYMjLA/project-details/8142143 accessed 9.11.2022
[26] https://reporter.nih.gov/search/DSSafL8TgkmP49MquyvTDQ/project-details/8313666 accessed 9.11.2022
[27] https://reporter.nih.gov/search/Ho2wtHWeYEyi7P9MQUkUtQ/projects accessed 9.11.2022

NIH also provided several hundred thousand dollars for research on the Nipah virus,[28] which has a 40-70% lethality rate, according to the WHO.[29]

Some of this money received by EcoHealth – about six hundred thousand dollars – was given as a subgrant to the Wuhan Institute of Virology, in spite of the fact that security issues in Chinese labs and specifically at the Wuhan Institute were well-known.

Several hundred pages of emails obtained as a result of a lawsuit filed by the White Coat Waste Project reveal significant information about Daszak and his partners. In an email to NIAID, Daszak lists several "Senior/Key Personnel" involved in his projects including Ralph Baric at the University of North Carolina Chapel Hill, and Shi Zhengli along with several other scientists at the Wuhan Institute of Virology.[30]

These emails also discuss collecting viruses from bats in several countries including Laos.[31] Why is this significant? The emails show that it was decided to send samples to the Wuhan Institute of Virology.

Viruses isolated from the bats from Laos were genetically very close to SARS-CoV-2; the only thing missing was the furin cleavage site. But it defies logic that a bat virus that is almost identical to SARS-CoV-2 could have been transported to the Wuhan lab, where gain of function research was taking place, that the outbreak of SARS-CoV-2 took place in Wuhan, and that this could all be a coincidence.[32] [33] [34] This is particularly unlikely in view of a grant proposal submitted by EcoHealth to another U.S. government agency that specifically referred to the "furin cleavage sites."

In 2018, Daszak, at EcoHealth Alliance, in partnership with Shi, Baric, and Linfa Wang director of the Programme in Emerging Infectious Diseases at Duke-N.U.S. Medical School), submitted a $14.2-million grant proposal to the U.S. Defense Advanced Research Projects Agency

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[28] https://reporter.nih.gov/search/DSSafL8TgkmP49MquyvTDQ/project-details/8326099
[29] https://www.who.int/news-room/fact-sheets/detail/nipah-virus
[30] Gain of Function Communications Between EcoHealth Alliance and NIAID p 21-22
[31] Gain of Function Communications Between EcoHealth Alliance and NIAID. P 61
[32] White Coat Waste Project. From Laos to Wuhan: ECW FOIA Investigation Sheds Light on Pandemic's Origins. December 7 2021 https://blog.whitecoatwaste.org/2021/12/07/from-laos-to-wuhan-wcw-foia-investigation-sheds-light-on-pandemics-origins/ accessed 9.10.2022
[33] Matt Riley. The COVID lab leak theory just got even stronger. *The Spectator* November 20 2021
[34] Wuhan scientists were studying Laos bat viral samples before COVID-Report. *Business Standard* November 22 2021 https://www.business-standard.com/article/current-affairs/wuhan-scientists-were-studying-laos-bat-viral-samples-before-covid-report-121112201019_1.html accessed 9.10.2022

(DARPA).[35] This proposal was ultimately turned down. But the proposal included plans to insert "human-specific" furin cleavage sites into SARS-like coronaviruses, and then to test the altered viruses in human respiratory cells and humanized mice. The furin cleavage site is particularly important since it is the most distinguishing feature of SARS-CoV-2. It allows the virus to bind more efficiently and release genetic material into human cells. It is one of the reasons that SARS-CoV-2 transmits so easily from human to human and can be so harmful.

According to Richard Ebright, molecular biologist at Rutgers University, "The relevance of this is that SARS-CoV-2…is the only virus in its entire genus of SARS-related coronaviruses that contains a fully functional cleavage site at the S1, S2 junction. And here is a proposal from the beginning of 2018, proposing explicitly to engineer that sequence at that position in chimeric lab-generated coronaviruses."[36]

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[35] https://www.documentcloud.org/documents/21066966-defuse-proposal accessed 9.10.2022
[36] Sharon Lerner, Maia Hibbet. Leaked Grant Proposal Details High Risk Coronavirus Research. *The Intercept* Sept 23, 2021 https://theintercept.com/2021/09/23/coronavirus-research-grant-darpa/ accessed 9.10.2022

Could SARS-CoV-2 Have Come From an Animal?

It is possible, but not probable. SARS was found to have been transmitted from bats to civets and then to humans in November 2002.[37] It took about four months to make this determination.[38] MERS emerged in Saudi Arabia in 2012 spread from bats to camels to people.[39] It took about nine months to make this determination.[40] But almost three years after the first patients were identified, no animal has been identified as the source of SARS-CoV-2. At this time, such a discovery is not likely to occur. Authors of a World Health Organization report wrote in an August letter to *Nature*, "The window is rapidly closing on the biological feasibility of conducting the critical trace-back of people and animals inside and outside China." Daszak was a co-author of this letter.[41]

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[37] Wang LF, Eaton BT. "Bats, civets and the emergence of SARS." *Curr Top Microl Immunol* 2007;315:325-344

[38] Guan Y, Zheng BJ, He YQ et al. "Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China." *Science* 2003 Oct;302(5643):276-278

[39] Han HJ, Yu H, Yu XJ. "Evidence for zoonotic origins of Middle East Respiratory syndrome coronavirus." *J Gen Virol* 2016 Feb;97(2):274-7280

[40] Omrani AS, Al-Tawfiq JA, Memish ZA. "Middle east respiratory syndrome coronavirus (MERS-CoV): animal to human interaction." *Pathog Glob Health* 2015 Dec;109(8):354-362

[41] Koopmans M, Dszak P, Dedkov VG et al. "Origins of the SARS-CoV-2: window is closing for key scientific studies." *Nature* 2021 Aug https://www.nature.com/articles/d41586-021-02263-6?proof=t%29Nature accessed 9.10.2022

Addressing the Myth That SARS-CoV-2
Originated at the Huanan Seafood Market

The first official announcement from the Chinese government concerning SARS-CoV-2 was issued on December 30, 2019, when the Wuhan Municipal Health Commission reported that "cases of pneumonia of unknown cause" were linked to the Huanan Seafood Market, which sold live wild animals in addition to seafood, including hedgehogs, badgers, snakes, and turtledoves. It was also stated there was no evidence of "obvious human to human transmission and no infection among medical personnel."[42]

Timeline for the Deception

On January 1, 2020, the Huanan Seafood Market was closed for cleaning. Vendors reported that workers had started spraying disinfectant on December 30, 2019.[43]

Scientists from China's National Institute for Viral Disease Control and Prevention collected 515 samples from the Huanan Seafood Market for analysis, also on January 1, 2020 and returned to collect 70 more samples from vendors after the market re-opened.

At the same time, an official at the Hubei Provincial Health Commission ordered gene sequencing companies and labs to stop testing and to destroy all patient samples.[44]

[42] Zhang Jingshu and Wang Ruiwen Editor: Li Jie. Wuhan Central Hospital claims that SARS rumors spread through the internet, there is no doubt that the patient may be diagnosed. *Beijing News* 12.31.2019 http://www.bjnews.com.cn/news/2019/12/31/668421.html accessed 9.10.2022
[43] Seafood market closed after outbreak of 'unidentified' pneumonia. *Global Times* Jan 1 2020 https://www.globaltimes.cn/content/1175369.shtml accessed 9.10.2022
[44] The Origins of the COVID-19 Global Pandemic, Including the Roles of the Chinese Communist Party and the World Health Organization. House Foreign Affairs Committee Minority Staff Interim Report. June 12. 2020 https://gop-foreignaffairs.house.gov/wp-content/uploads/2020/08/Interim-Minority-Report-on-the-Origins-of-the-COVID-19-Global-Pandemic-Including-the-Roles-of-the-CCP-and-WHO-8.17.20.pdf accessed 9.10.2022

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On January 2, 2020 an analysis of samples from patients at Wuhan's Jinyintan Hospital by researchers at Wuhan Institute of Virology identified the novel coronavirus.[45]

On January 3, 2020 the Wuhan Municipal Commission reported that 44 patients had been identified with symptoms consistent with "pneumonia of unknown origin" some of whom worked at the Huanan Seafood Wholesale Market and 11 of whom were severely ill.[46]

On January 5 2020
A WHO statement was posted that included the following:

> "The reported link to a wholesale fish and live animal market could indicate an exposure link to animals. The symptoms reported among the patients are common to several respiratory diseases, and pneumonia is common in the winter season; however, the occurrence of 44 cases of pneumonia requiring hospitalization clustered in space and time should be handled prudently."[47]
>
> According to the authorities, some patients were operating dealers or vendors in the Huanan Seafood market. Based on the preliminary information from the Chinese investigation team, no evidence of significant human-to-human transmission and no health care worker infections have been reported.[48]

The WHO also posted this statement:

> The reported link to a wholesale fish and live animal market could indicate an exposure link to animals. The symptoms reported among the patients are common to several respiratory diseases, and pneumonia is common in the winter season; however, the occurrence of 44 cases of pneumonia requiring hospitalization clustered in space and time should be handled prudently.[49]

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[45] Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19) 16-24 Feb 2020 https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf accessed 9.10.2022
[46] Lu H, Stratton CW, Tang YW. "Outbreak of Pneumonia of Unknown Etiology in Wuhan China: The mystery and the miracle." *J Med Viro* 2020 Apr;92(4):401-402
[47] IBID
[48] World Health Organization. Pneumonia of unknown cause – China. World Health Organization https://www.who.int/csr/don/05-january-2020-pneumonia-of-unkown-cause-china/en/ accessed 9.10.2022
[49] IBID

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In other words, the WHO was repeating the Chinese claim that the virus originated in the seafood market and gave the impression that there was no reason for concern.

January 12, 2020
WHO issued this statement: "China shared the genetic sequence of the novel coronavirus on 12 January, which will be of great importance for other countries to use in developing specific diagnostic tests." WHO also stated, "The evidence is highly suggestive that the outbreak is associated with exposures in one seafood market in Wuhan. The market was closed on 1 January 2020. At this stage, there is no infection among healthcare workers, and no clear evidence of human-to-human transmission."[50]

January 14, 2020
WHO tweets, "Preliminary investigations conducted by the Chinese authorities have found no clear evidence of human-to-human transmission of the novel #coronavirus (2019-nCov) identified in #Wuhan, #China."[51]

January 26, 2020
The Institute of Virology and Chinese CDC announced that the novel coronavirus was present in 33 of the 585 environmental samples collected from the Wuhan Huanan Seafood Wholesale Market earlier in the month. Of these 33 samples, all but two were collected from an area of the market where wildlife vendors were located. Xinhua News Service says the results indicate "the virus stems from wild animals on sale at the market."[52]

Almost immediately, however, published research showed that the market could not have been the source of the outbreak. The co-authors of an article published in the *Lancet*, including experts from Wuhan's leading infectious disease hospital, reported that among the first 41 patients identified in Wuhan, the first patient to show symptoms, on December 1, 2019, had no exposure to the market. Two of the next three patients to show symptoms, all on December 10, also had no exposure to the market. "No epidemiological link was found between the first patient and later cases," the researchers wrote. And, in fact, there were 13 patients with no link to the market.[53]

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50 Novel Coronavirus—China. World Health Organization. January 12, 2020 https://www.who.int/emergencies/disease-outbreak-news/item/2020-DON233 accessed 9.10.2022
51 https://twitter.com/WHO/status/1217043229427761152 accessed 9.10.2022
52 China Detects Large Quantity of Novel Coronavirus at Wuhan Seafood Market. *XinhuaNet* January 27, 2020 http://www.xinhuanet.com/english/2020-01/27/c_138735677.htm accessed 9.10.2022
53 Huang C, Wang Y, Li X et al. "Clinical Features of Patients Infected with 2019 Novel Coronavirus in Wuhan, China." *Lancet,* 2020 Feb;395(10223):P497-506

"That's a big number, 13, with no link," stated Daniel Lucey, an infectious disease specialist at Georgetown University, who went on to say that the *Lancet* paper raised questions about the overall accuracy of the data the CCP was providing to the world.

According to Lucey, the Wuhan Municipal Health Commission was the "official source" of public information and on January 11, 2020, reported that there were only 41 confirmed patients, that there was no evidence of human-to-human transmission, and that most cases were related to the market. Because the Wuhan Municipal Health Commission noted that diagnostic tests had confirmed these 41 cases by January 10, 2020, and officials presumably knew the case histories of each patient, Lucey said "China must have realized the epidemic did not originate in that Wuhan Huanan seafood market."[54]

An article published in the *Lancet* on January 30, 2020 reported that of 99 patients diagnosed with COVID-19 between Jan 1 and Jan 20, 2020, forty-nine had been exposed to the Huanan Seafood Market, and 50 had not.[55] And an article in the *New England Journal of Medicine* reported that of 425 confirmed cases, the majority (55%) with onset before January 1, 2020 were linked to seafood market, although this was true for only 8.6% of subsequent cases.[56] The theory that the seafood market was the source of the outbreak and that the virus was not transmissible between humans was falling apart.

It is important to note that the First National Health Commission arrived in Wuhan December 31, 2019, and determined that in order to diagnose SARS-CoV-2, three criteria needed to be met: **a history of exposure to the seafood market**, fever, and the full genome from respiratory or serum specimens identical to SARS-CoV-2 sequences.[57]

The timeline above, however, indicates that the Chinese knew that one third had no contact with the seafood market when these criteria were established. So why were these criteria established? To mislead the world about the origin of the virus? The criteria were not changed until January 18, 2020, but on January 26, 2020, Chinese authorities were still claiming that the virus originated at the seafood market.

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[54] Jon Cohen. Wuhan seafood market may not be source of novel virus spreading globally. *Science* Jan 26 2020 https://www.sciencemag.org/news/2020/01/wuhan-seafood-market-may-not-be-source-novel-virus-spreading-globally accessed 9.10.2022

[55] Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y. "Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study." *Lancet* 2020 Feb;395(10223):P507-513

[56] Li Q, Med M, Guan X et al. "Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia." *NEJM* 2020 Mar;382:1199-1207

[57] Han Y, Yang H. "The transmission and diagnosis of 2019 novel coronavirus infection disease (COVID-19): A Chinese perspective." *J Med Virol* 2020 Mar;92:639-644

So where *did* this virus originate?

A sample of bronchoalveolar fluid from a single patient hospitalized on December 26, 2019, identified a new RNA virus strain most closely related (89.1% nucleotide similarity) to a group of SARS-like coronaviruses previously found in bats in China. The researchers noted that although SARS-like viruses have been identified widely in bats in China, viruses identical to SARS-CoV had not yet been documented. They noted that the Wuhan coronavirus was most closely related to bat coronaviruses and showed 100% amino acid similarity to bat SL-CoVZC45 in the nsp7 and E proteins. [58] The problem is that there were no bats at the seafood market, which means that the virus could not have originated there.

In a paper published in the *Lancet,* researchers wrote, "Notably, 2019-nCoV was closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21, collected in 2018 in Zhoushan, in eastern China."[59] The researchers were referring to a 2018 paper which reported the results of an analysis of 334 bats collected between 2015 and 2017 from Zhoushan City in Zhejiang province China. Coronaviruses were detected in 26.65% of these bats, and the viruses had 81% shared nucleotide identity with human/civet SARS-CoVs.[60] This sounds complicated, and it is, but what this means is that the Wuhan virus was very similar to bat viruses. Yet there were no bats at the seafood market. Also remember that "the bat lady" – Shi - had been studying bat viruses at the WIV for an exceptionally long time.

Again, the CCP was not forthcoming. The Shanghai lab where researchers published the first genome sequence of the coronavirus that caused COVID-19 was shut down by the Shanghai Health Commission for "rectification" on January 12, 2020, five days after Professor Yong-Zhen Zhang's team published the genome sequence and made it available to the public. The team had reported that the virus resembled a group of viruses previously found in bats. This lab was a Level 3 biosafety facility and had just passed its annual inspection on January 5, 2020.[61]

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[58] Wu F, Zhao S, Yu B et al. "A new coronavirus associated with human respiratory disease in China." *Nature* 2020 Feb;579:265-269
[59] Lu R, Zhao X, Li J et al. "Genomic characterization and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding." *Lancet* 2020 Feb;395:565-574
[60] Hu D, Zhu C, Ai L et al. "Genomic characterization and infectivity of a novel SARS-like coronavirus in Chinese bats." *Emerg Microbes Infect* 2018 Sep;7:154
[61] Zhuang Pinghui "Chinese laboratory that first shared coronavirus genome with world ordered to close for 'rectification', hindering its Covid-19 research." *South China Morning Post* Feb 28 2020 https://www.scmp.com/news/china/society/article/3052966/chinese-laboratory-first-shared-coronavirus-genome-world-ordered accessed 9.10.2022

Indian researchers also studied the virus and found four insertions in the spike protein that are unique to SARS-CoV-2 and not present in other coronaviruses. The amino acid residues in all four insertions were found to be similar to amino acid residues in the structural proteins of HIV-1. The researchers noted that there are only 3 viruses that contain these sequences – HIV-1, the bat coronaviruses discovered by Shi, and the New Wuhan virus (COVID-19). They also noted that it was highly unlikely that this could have occurred naturally.[62]

This article was later withdrawn. The Indian researchers wrote that they intended to revise it in response to comments received from the research community.[63] Almost a year later, Ashutosh Kumar Pandey, one of the researchers, told a reporter that the article was inconvenient for those who wanted to promote the natural origin theory. He stated that the paper was withdrawn due to pressure from "people with vested interests."

Pandey also said that the original paper represented a small portion of the studies that he and his group had conducted. When they tried to include their entire findings in a new article, the revised manuscript was blocked by journal publishers. When asked how it was possible for scientific papers to be blocked to comply with a particular agenda, he replied, "Science is the new medieval church, those who are popes of it censor at their will."[64]

Notes from a lecture delivered by Shi shortly before the outbreak began disappeared from the Institute website.

The CCP's order to labs to destroy samples, and its refusal to share information and samples to the world community has not helped to instill confidence in the integrity of Chinese officials and their representations concerning the virus.

Bottom Line: What we now call SARS-CoV-2 is almost identical to viruses obtained from bats in Laos and shares important characteristics with chimeric viruses created via gain-of-function research. There is almost no evidence to support the idea that this virus was transmitted directly from bats or other animals to humans, or that the original patients were infected at the wet market.

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[62] Pradhan P, Pandley AK, Mishra A et al. "Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag." *BioRxiv* https://doi.org/10.1101/2020.01.30.927871
[63] IBID
[64] COVID-19 lab leak theory: Indian scientists had flagged 'unnatural insertions' in its genome, were forced to withdraw study. *OpIndia* June 4 2021 https://www.opindia.com/2021/06/indian-scientists-had-found-unique-insertions-in-covid-19-virus-genome/ accessed 9.10.2022

Conclusion: The Creation of SARS CoV-2 Was Funded by NIH, NIAID, and EcoHealth Alliance and Took Place in a Lab

A comparison between a virus created in a lab, and described in a paper published in *Nature Medicine* reveals startling similarities to SARS-CoV-2:[65]

- Younger mice were relatively unaffected.
- The virus was deadly to older mice or mice with compromised immune systems.
- Showed strong tendency to attack lung tissue, invade human bronchial epithelial cells.
- Caused weight loss in mice, a common side effect of SARS-CoV-2 in humans.
- Resistant to standard treatment.
- Researchers were unable to develop an effective vaccine.
- When a vaccine made of "inactivated whole SARS-CoV" was given to older animals they became sicker when re-exposed to SARS-CoV.
- Older animals vaccinated and then exposed: "augmented immune pathology was also observed, indicating the possibility of the animals being harmed because of the vaccination."
- Exaggerated immune response after vaccination and re-exposure.

According to the article, this work was funded by EcoHealth Alliance, The National Institute of Allergy and Infectious Diseases (NIAID), and The National Institutes of Health. The authors of the paper included Zhengli-Li Shi (from the Wuhan Institute), Ralph Baric (UNCH) and Peter Daszak (EcoHealth Alliance).

Another clue as to the origin of SARS-CoV-2 comes from an interview with Daszak conducted by virologist Vincent Racaniello on December 19, 2019, just three weeks before the Wuhan Municipal Health Commission reported the first cases of what turned out to be COVID-19:

[65] Menachery VD, Yount BL, Debbink K et al. "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence." *Nat Med* 2015 Nov;21:1508-1513

At the 28:10 mark of the podcast interview, Daszak states that researchers found that SARS likely originated from bats and then set out to find more SARS-related coronaviruses, eventually finding over one hundred of them.

Daszak reported that some coronaviruses can "get into human cells in the lab," and others can cause SARS disease in "humanized mouse models."

He warned that such coronaviruses are "untreatable with therapeutic monoclonals [antibodies] and you can't vaccinate against them with a vaccine."

Daszak claimed that his team's goal was trying to find the next "spillover event" that could cause the next pandemic.

At the 29:54-mark Daszak is asked what can be done to deal with coronaviruses given that there are no therapeutics or vaccines for them, Daszak discusses that the goal of his GoF (gain-of-function) research was to develop a universal vaccine that could be used for many different types of coronaviruses.

Referring specifically to bat coronaviruses, Daszak said, "You can manipulate them in the lab pretty easily." He then mentioned the most unique characteristic of SARS-CoV-2 (which had not yet been named at the time of this podcast), the spike protein, stating "Spike protein drives a lot of what happens with the coronavirus, zoonotic risk." He also talked about inserting the spike protein "into a backbone of another virus" and then doing "some work in the lab."

Daszak acknowledged collaboration with Baric: "and we work with Ralph Baric at UNC [University of North Carolina] to do this."

Daszak also admitted the creation of chimeras in order to investigate vaccines: "Now, the logical progression for vaccines is, if you are going to develop a vaccine for SARS, people are going to use pandemic SARS, but let's try to insert these other related diseases and get a better vaccine."[66]

Evidence also shows that SARS-CoV-2 is likely not only manmade but may have been developed in collaboration with other entities.

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[66] Keoni Everington. WHO inspector caught on camera revealing coronavirus manipulation in Wuhan before pandemic. *Taiwan News* Jan 18 2021 https://www.taiwannews.com.tw/en/news/4104828 accessed 9.10.2022

BLAST is an acronym for Basic Local Alignment Search Tool. It's a computer algorithm available for use at the National Center for Biotechnology Information (NCBI) website. The algorithm allows scientists to quickly query a DNA sequence to find matches or regions of similarity between protein sequences. Scientists worldwide deposit their sequences when they make new discoveries.

A distinguishing feature of SARS-CoV-2 is the furin cleavage site and the 12- nucleotide insertion in the spike protein, particularly its two consecutive CGG codons. Researchers conducted a BLAST search and found a 100% reverse match in a proprietary U.S. patent filed on February 4, 2016 (US patent 9,587,003).[67] According to the researchers, statistical analysis shows that the probability of this sequence randomly being present in a 30,000-nucleotide viral genome is 3.21×10^{-11} (less than one in one billion). The owner of the patent is Moderna, which makes COVID-19 vaccines using mRNA technology.[68]

While nothing is impossible, a SARS virus mutating in nature and jumping species that contains a furin cleavage site that does not exist in nature but does exist in a Moderna patent – not at all likely. The authors write, "The presence in SARS-CoV-2 of a 19-nucleotide sequence encoding an FCS at amino acid 681 of its spike protein with 100% identity to the reverse complement of a proprietary MSH3 mRNA sequence is highly unusual. Potential explanations for this correlation should be further investigated."[69]

[67] Bancel S, Chakraborty T, De Fougerolles A, Elbashir SM, John M, Roy A, et al. *Modified Polynucleotides for the Production of Oncology-Related Proteins and Peptides*. Cambridge, MA: United States Patent. (2016). https://pubchem.ncbi.nlm.nih.gov/patent/US-9587003-B2 accessed 9.10.2022
[68] Ambati BK, Varshney A, Lundstrom K et al. "MSH3 Homology and Potential Recombination Link to SARS-CoV-2 Furin Cleavage Site." *Frontiers Virol* 2022 Feb; https://doi.org/10.3389/fviro.2022.834808 accessed 9.10.2022
[69] IBID

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The Cover-Up

Peter Daszak, Anthony Fauci, and many others have invested considerable effort in trying to convince the public and the scientific community that the lab origin theory is false.

In February 2020, Daszak organized scientists to write an open letter published in the *Lancet* that included these statements: "The rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins. We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin."[70]

Daszak was one of the authors. But prior to signing on, he expressed concern about distancing himself to hide his participation in gain-of-function research. In an email obtained through a Freedom of Information Act request, Daszak wrote to collaborator Ralph Baric: "I spoke with Linfa [Wang] last night about the statement we sent round. He thinks, and I agree with him, that you, me, and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way. We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice."[71]

Baric agreed, writing back, "I also think this is a good decision. Otherwise it looks self-serving and we lose impact."[72]

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[70] Calisher C, Carroll D, Colwell R et al. "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19." *The Lancet* 2020 Mar;395(10226):E42-E43
[71] Emails show scientists discussed masking their involvement in key journal letter on COVID origins. US Right to Know Feb 15 2021 https://usrtk.org/biohazards-blog/scientists-masked-involvement-in-lancet-letter-on-covid-origin/ accessed 9.10.2022
[72] IBID

The letter included this statement: "We declare no competing interests."[73] Daszak also told the *Washington Post* that he had no conflicts of interest concerning his work with Shi Zhengli at the Wuhan Institute of Virology.[74]

Daszak further tried to cover his tracks when he agreed to be part of a team sent to China by the World Health Organization in February 2021 to investigate the origin of SARS-CoV-2. Not surprisingly, the team reported that it was "extremely unlikely" that the virus has been released from a lab.[75] Team members were asked to sign a declaration of interest and according to the report, "All declared interests were assessed and found not to interfere with the independence and transparency of the work."[76] It is difficult to believe that Dasak could have disclosed his connection to the Wuhan Institute and gain-of-function research and met the criteria for "independence and transparency."

Daszak also hid his conflicts of interest concerning his research and his ties to the Wuhan Institute of Virology from Jeffrey Sachs, chair of the *Lancet* COVID-19 Commission. Daszak had been asked by Sachs to head a Task Force to look into the origins of COVID-19. According to Sachs, "It is clear that the NIH co-funded research at the Wuhan Institute of Virology that deserves scrutiny under the hypothesis of a laboratory-related release of the virus."[77] Sachs ended the task force's work after more information became public that questioned the veracity of statements made by Daszak.[78]

Daszak's collaborators are equally evasive. According to David Morens, Daszak's work benefits humanity and we should all be grateful."[79] But Morens is with the National Institute

[73] Calisher C, Carroll D, Colwell R et al. "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19." *The Lancet* 2020 Mar;395(10226):E42-E43
[74] Josh Rogin. Opinion: the coronavirus shows he risks of scientific collaboration with China. *Washington Post* Apr 23 2020 https://www.washingtonpost.com/opinions/global-opinions/the-coronavirus-crisis-shows-the-risks-of-scientific-collaboration-with-china/2020/04/23/4ccd5850-85a8-11ea-878a-86477a724bdb_story.html accessed 9.10.2022
[75] WHO-convened Global Study of the Origins of SARS-CoV-2: China Part. file:///C:/Users/Pam/Downloads/Final-joint-report_origins-studies-6-April-201%20(2).pdf accessed 9.10.2022
[76] IBID p 12
[77] Jeffrey Sachs. Finding the Origins of the COVID-19 and Preventing Future Pandemics. https://www.jeffsachs.org/newspaper-articles/cp24mtcpswgyty5st4pm29mwh6dt2d accessed 9.10.2022
[78] COVID-19: *Lancet* investigation into origin of pandemic shuts down over bias risk. *BMJ* 2021;375:n2414
[79] Jon Cohen. Prophet in Purgatory. *Science* November 17 2021

of Allergy and Infectious Diseases, which provides grant money to Daszak, and he co-authors articles defending the idea that SARS-CoV-2 came from nature.[80]

Yet more evidence of a cover-up is described in email exchanges between Anthony Fauci, head of the National Institute of Allergy and Infectious Diseases, other NIH personnel and outside researchers.

On January 31, 2020, Fauci received an email from Greg Folkers of the National Institutes of Health.[81] The email included no text, but an article published in *Science* was attached.[82] This article reported that scientists were sharing and reviewing a growing number of genetic sequences of the virus obtained from infected patients. These had been posted in the Global Initiative on Sharing All Influenza Data database.[83] The author reported that there was some doubt as to whether the virus originated in the wet market, which was the story promoted by U.S. and Chinese authorities at the time. The author also reported that many scientists had been expressing concerns for many years about experiments conducted at the Wuhan Institute and cited the gain-of-function research fully described in the above-mentioned article in *Nature Medicine* in 2015.[84] This article included a disclosure that the research was funded by the National Institute of Allergy and Infectious Diseases (NIAID), the division of the NIH headed by Fauci, along with the NIH and EcoHealth.

Within minutes, Fauci forwarded the *Science* article to Jeremy Farrar, the head of Wellcome Trust, a UK non-profit, and Kristian Andersen with Scripps Research Institute.[85] He later sent the article to Robert Kadlec at the Health and Human Services Office of the Assistant Secretary for Preparedness and Response.[86]

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80 Morens D, Daszak P, Markel H, Taubenberger JK. "Pandemic COVID-19 Joins History's Pandemic Legion." *mBio* 2020 May;11(3):e00812-20

81 https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3229 accessed 9.10.2022

82 Jon Cohen. Mining coronavirus genomes for clues to the outbreak's origins. *Science* Jan 31 2020

83 https://gisaid.org/database-features/flusurver-mutations-app/ accessed 9.10.2022

84 Menachery VD, Yount BL, Debbink K et al. "A SARS-like cluster of circulating bat coronaviruses shows great potential for human emergence." *Nature Medicine* 2015 Nov;21:1508-1513

85 https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3187 accessed 9.10.2022

86 https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3222 accessed 9.10.2022

On the same day, Kristian Anderson wrote in an email to Fauci: "The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered."[87]

The next day on February 1 2020, Fauci sent an email to Hugh Auchincloss, deputy director of NIAID.[88] The subject line was IMPORTANT (in all caps) and read: "It is essential that we speak this AM. Keep your cell phone on…Read this paper as well as the email that I will forward to you now. You will have tasks today that must be done."
Attached to the second email was a document titled "Baric, Shi et al – Nature Medicine – SARS Gain of Function.pdf." This is particularly important since Fauci denied under oath in front of a Senate hearing that Ralph Baric was conducting gain-of-function research at the University of North Carolina. Within a few seconds, Fauci forwarded the article from *Science*[89] to Auchincloss as well.[90] He then forwarded the *Nature Medicine* article to Lawrence Tabak at the National Institutes of Health with "IMPORTANT" in the memo.[91]

It seems that Fauci was concerned and was alerting his colleagues that disclosure of this information might be a problem. The others seemed equally concerned. Farrar sent an email at 10:34AM announcing that he had scheduled a conference call and wrote that his expectation was that "information and discussion is shared in total confidence and not to be shared until agreement on next steps."[92]

Auchincloss then wrote to Fauci, "The paper you sent me says the experiments were performed before the gain of function pause but have since been reviewed and approved by NIH. Not sure what that means since Emily is sure that no Coronavirus work has gone through the P3 framework. She will try to determine if we have any distant ties to this work abroad."[93] Fauci replied, "OK. Stay tuned."[94]

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[87] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p 3187 accessed 9.10.2022
[88] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p 3221 accessed 9.10.2022
[89] Jon Cohen. Mining coronavirus genomes for clues to the outbreak's origins. *Science* Jan 31 2020
[90] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p 3215 accessed 9.10.2022
[91] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3210 accessed 9.10.2022
[92] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3197 accessed 9.10.2022
[93] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3206 accessed 9.10.2022
[94] https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3206 accessed 9.10.2022

During the conference call, Farrar sent an email to four of the people on the call, including Fauci, that read, "Can I suggest we shut down the call and then redial in? Just for 5-10 minutes?"[95]

There are several follow-up emails between the parties but the most important are those that discuss the need to talk to World Health Organization Director-General Tedros. An email of particular interest is from Farrar to Fauci and NIH Director Collins, which was shared with others: "Tedros and Bernhard have apparently gone into conclave … they need to decide today in my view. If they do prevaricate, I would appreciate a call with you later tonight or tomorrow to think how we might take forward [sic]."[96] In this email, Farrar expressed concern about an article published by ZeroHedge which discussed the potential lab release as the origin of the virus.[97] Subsequently ZeroHedge was banned from Twitter.

On February 3 2021, Tedros delivered a Report of the Director-General, 146th Meeting of the Executive Board, during which he emphasized the importance of controlling the spread of misinformation and announced that WHO was working with Google **"**to make sure people searching for information about coronavirus see WHO information at the top of their search results. Social media platforms including Twitter, Facebook, Tencent and Tiktok have also taken steps to limit the spread of misinformation."[98] The proper term to describe this might be "censorship."

In March 2020, a statement of support for the idea that SARS-CoV-2 was transmitted from an animal to a human was published in the *Lancet*.[99] It was signed by many people including Peter Daszak, President of EcoHealth Alliance and Christian Drosten. Then things start to get very interesting.

EcoHealth Alliance is the organization that received money from NIAID and distributed it to Ralph Baric at the University of North Carolina Chapel Hill, and Shi Zhengli, a virologist

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95 https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p 3172 accessed 9.10.2022

96 96 https://assets.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf p3125 accessed 9.10.2022

97 Tyler Durden. Coronavirus Contains "HIV Insertions", Stoking Fears Over Artificially Created Bioweapon. *ZeroHedge* Feb 1 2020

98 Report of the Director-General, 146th Meeting of the Executive Board. https://www.who.int/director-general/speeches/detail/report-of-the-director-general-146th-meeting-of-the-executive-board accessed 9.10.2022

99 Calisher C, Carroll D, Colwell R et al. "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19." *Lancet* 2020 Mar;395(10226):E42-E43

referred to as the "bat lady" at the Wuhan Institute of Virology. The money was earmarked for gain-of-function research. Emails obtained by U.S. Right to Know show that the "statement of solidarity" that appeared in the *Lancet* was actually drafted by Peter Daszak.[100]

Apparently, Ralph Baric was shown drafts of Daszak's letter but was informed by Daszak that he did not need to sign the statement. Baric agreed, stating that doing so would appear to be self-serving. Daszak wrote that other key people would be looking at the letter and that it would be "…put out in a way that doesn't link it back to our collaboration so we maximize an independent voice."[101] Daszak also wrote, "Please note that this statement will not have EcoHealth Alliance logo on it and will not be identifiable as coming from any one organization or person, the idea is to have this as a community supporting our colleagues."[102] This shows deliberate intent to hide the relationships between the parties. Indeed, five of the signers of this "solidarity statement" were directly affiliated with EcoHealth Alliance[103] and two were partners of EcoHealth.[104]

Christian Drosten is another signer of the solidary statement. He also has an interesting background. Drosten and his colleagues had published an article in *Eurosurveillance* on Jan 23, 2020, in which they claimed to have developed a RT-PCR test for SARS-CoV-2.[105] There were several problems with this paper, including the fact that that this group did not have SARS-CoV-2 viral material at the time that the article was published. The researchers acknowledged this, writing: "We aimed to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available."[106] Instead, the group relied on theoretical sequences which were provided by a lab in China. Despite this, the test was immediately endorsed by World Health Organization Director General Tedros Adhanom. A large group of scientists has called for this paper to be retracted for many reasons, including undisclosed conflicts of interest for some of the authors and lack of peer review.[107]

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[100] https://usrtk.org/wp-content/uploads/2020/11/Biohazard_FOIA_Maryland_Emails_11.6.20.pdf accessed 9.10.2022
[101] https://usrtk.org/wp-content/uploads/2021/02/Baric_Daszak_email.pdf p 273 accessed 9.10.2022
[102] https://usrtk.org/wp-content/uploads/2021/02/Baric_Daszak_email.pdf p 274 accessed 9.10.2022
[103] Sainath Suryanarayanan. EcoHealth Alliance orchestrated key scientists statement on "natural origin" of SARS-CoV-2. *USRTK* Nov 18 2020 https://usrtk.org/biohazards-blog/ecohealth-alliance-orchestrated-key-scientists-statement-on-natural-origin-of-sars-cov-2/ accessed 9.10.2022
[104] https://www.ecohealthalliance.org/partners
[105] Corman VM, Landt O, Kaiser M et al. "Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR." *Euro Surveill* 2020 Jan;25(3):2000045
[106] IBID
[107] Borger P, Malhotra BR, Yeadon M et al. "External peer review of the RTPCR test t detect SARS-CoV-2 reveals 10 major scientific flaws at the molecular and methodological level: consequences for false positive results." Corman-Drosten Review Report. November 27 2020 https://cormandrostenreview.com/report/ accessed 9.10.2022

The bottom line: both Daszak and Drosten had significant motivation to keep the actual origin of the virus, their knowledge about it, and other details a secret; as did Fauci and other employees of the NIH and NIAID.

Kristian Andersen, who had, in late January, written to Fauci expressing his concerns that SARS-Co-V-2 included sequences that appeared to be manmade, led a group that published an article in *Nature* on March 17, 2020, in support of the theory that the virus was transmitted from animals to humans.[108] After this, Andersen received a generous grant from the National Institutes of Health. At this time, we have no way of knowing if this was a form of quid pro quo, but it can at least be said that this does not pass the "smell test."

Dr. Anthony Fauci continued to insist that gain-of-function research was not responsible for the creation of SARS-CoV-2 and stated under oath when testifying in front of a Senate Committee that neither his agency nor the National Institute of Health funded gain-of-function research. In response to questions from Senator Rand Paul he said, "With all due respect, you are entirely, completely incorrect." He added that the NIH "…has not and does not now fund gain-of-function research in the Wuhan Institute of Virology."[109]

But The National Institutes of Health admitted that it funded gain-of-function research on bat coronaviruses at the Wuhan Institute in China. In a letter to Rep James Comer (R-KY), NIH Deputy Director Lawrence Tabak stated that the NIH had given a grant to EcoHealth Alliance Inc which then awarded a subgrant to the Wuhan Institute of Virology, and that EcoHealth had failed to submit reports as required under the terms of the grant. In this letter, Tabak stated that EcoHealth's "limited experiment" looked at whether spike proteins from naturally occurring bat viruses circulating in China were capable of binding to the ACE2 receptor in a mouse model. Tabak stated that mice infected with the modified virus became sicker than those who were infected with the unmodified virus. Tabak also wrote, "As sometimes occurs in science, this was an unexpected result of the research, as opposed to something that the researchers set out to do."[110]

A letter dated Oct 27, 2021, from Congressional leaders to Frances Collins, (former) Director of the National Institutes of Health, concerned inadequate oversight of grants made from NIH to

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[108] Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. "The proximal origin of SARS-CoV-2." *Nature Medicine* 2020 Mar;26:450-452

[109] Jack Brewster. Fauci and Sen Rand Paul Spar Over Wuhan Lab Research and COVID-19 Origin. *Forbes* May 11 2021 https://www.forbes.com/sites/jackbrewster/2021/05/11/fauci-and-sen-rand-paul-spar-over-wuhan-lab-research-and-covid-19-origin/?sh=5169857e1df9 accessed 9.10.2022

[110] Emily Crane. NIH admits US funded gain-of-function in Wuhan – despite Fauci's denials. *New York Post* Oct 21 2021 https://nypost.com/2021/10/21/nih-admits-us-funded-gain-of-function-in-wuhan-despite-faucis-repeated-denials/ accessed 9.10.2022

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EcoHealth Alliance. Some of these concerns arose from a bipartisan "in camera" review of documents conducted at the Department of Health and Human Services (DHHS). The documents were examined in chambers because the NIH refused to make the documents public.

Here are excerpts from this letter to Dr. Collins:

> NIH terminated an EcoHealth Alliance grant in April 2020, reinstated the grant and then suspended the grant in July 2020 due to EcoHealth's inadequate oversight of research at the Wuhan Institute of Virology.
>
> EcoHealth Alliance refused to provide information to the NIH related to its subaward to the Wuhan Institute of Virology.
>
>> NIH failed to report EcoHealth's noncompliance and grant suspension into the www.SAM.gov database that alerts other U.S. Government agencies to risky grant recipients.
>>
>> Both Daszak and officials at the National Institute of Allergy and Infectious Disease appeared to have known that EcoHealth's research was crossing the line in consideration of the moratorium on gain-of-function research. In a 2016 project report concerning to the NIH concerning his research, EcoHealth described its plans to carry out experiments involving humanized mice using two chimeric bat coronaviruses.[111]
>>
>> Subsequently NIH wrote to EcoHealth, stating that the research studies appeared "to involve research covered under the pause."
>
> Daszak replied on behalf of EcoHealth Alliance, and asserted that the organization's research did not involve gain of function:
>
>> "These 2 chimeric bat-like CoVs were constructed on Sept. 24, 2015. They use the backbone of a group 2b SARS-like bat CoV WIV1 and the spike proteins of two newly discovered bat SL-CoVs (Rs7327 and RsSHC014). The construction of these chimeric viruses aims to understand the receptor usage and infectivity of bat SL-CoVs that may be progenitors of SARS-CoV. We have not yet tested the pathogenicity of these viruses in animals."

[111] Understanding the Risk of Bat Coronavirus Emergency. Project Number 5R01AI110964-04 https://reporter.nih.gov/search/H_f9L5dZYESM-o4gIMrLig/project-details/9320765

Daszak offered no explanation concerning how RsSHC014 differed from the RsSCHO14 spike protein that was reported to be of great concern in 2015.[112]

Instead, Daszak stated that this work would not be considered GoF because "…the pause specifically targeted experiments that related to the pathogenicity or transmissibility of SARS-CoV, MERS CoV and any influenza virus. Our molecular clone is WIV1, which is a group 2b SARS-like bat coronavirus that has never been demonstrated to infect humans or cause human disease." But this was not true.

> Gain of function research funded by the National Institute of Allergy and Infectious Diseases and the National Institute of Aging of the NIH concluded: "…viruses using the WIV1-CoV spike protein are capable of infecting HAE cultures directly without further spike adaptation. Whereas in vivo data indicate attenuation relative to SARS-CoV, the augmented replication in the presence of human *ACE2* in vivo suggests that the virus has significant pathogenic potential…"[113]
>
> "…studies that build reagents based on viruses from animal sources cannot exclude the possibility of increased virulence or altered immunogenicity that promote escape from current countermeasures. As such, the potential of a threat, real or perceived, may cause similar exploratory studies to be limited out of an "abundance of caution."[114]
>
> "…the WIV1-CoV cluster has been identified as a threat for future emergence in human populations due to robust replication in primary human airway epithelial cell cultures."[115]

In other words, WIV1 was known to be potentially dangerous to humans.

Daszak proposed that Daszak/EcoHealth and its collaborators would immediately stop their research and inform their NIAID program officer if the chimeras showed evidence of virus growth greater than 1 log (or 10 times) the growth rate of the original viruses and/or grow more efficiently in human lung cells.

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[112] Menachery VD, Yount BL, Sims AC et al. "SARS-like WIV1-CoV poised for human emergence." *PNAS* 2016 Mar;113(11):3048-3053
[113] Menachery VD, Yount BL, Sims AC et al. "SARS-like WIV1-CoV poised for human emergence." *PNAS* 2016 Mar;113(11):3048-3053
[114] IBID
[115] IBID

Ignoring obvious warning signs, NIAID agreed with EcoHealth's self-assessment and agreed to let EcoHealth police its own activities. A NIH July 7, 2016, response letter to EcoHealth included these statements:

> NIAID is in agreement that the work proposed under Aim 3 to generate MERS-like or SARS-like chimeric coronaviruses (CoVs) is not subject to the GoF research funding pause. This determination is based on the following: (1) the chimeras will contain only S glycoprotein genes from phylogenetically distant bat CoVs; and (2) recently published work demonstrating that similar chimeric viruses exhibited reduced pathogenicity. Therefore, it is not reasonably anticipated that these chimeric viruses will have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route.

As a result, the NIAID added the following award condition, per the grant documents (NOTE: this is the specific language proposed by Daszak to NIAID):

> NIAID acknowledges that if any of the MERS-like or SARS-like chimeras generated under this grant show **evidence of enhanced virus growth greater than 1 log over the parental backbone strain**, Dr. Daszak will immediately stop all experiments w/ these viruses and provide the NIAID Program Officer and Grants Management Specialist, and Wuhan Institute of Virology Institutional biosafety Committee, with the relevant data and information related to these unanticipated outcomes. (Emphasis added).[116]

Daszak and EcoHealth did not do what they promised. Sometime during the period June 2017-May 31, 2018, the experiments involving chimeric viruses and humanized mice were carried out. EcoHealth and the Wuhan Institute of Virology infected humanized mice with the WIV1 parental virus and three chimeric viruses containing SHC014S, WUV16S and Rs4231S. The SHC014S virus grew at 10,000 times greater than the parent virus. Mice lost 20% of the body weight in six days.

At day two and four, "Viral loads in lung tissues of mice challenged with all three chimeras reached >10^6 genome copies per/g, significantly higher than related WIV1 infection (Fig. 6b). This demonstrates that pathogenicity of SARS-related coronaviruses in humanized mice differs

[116] https://republicans-energycommerce.house.gov/wp-content/uploads/2021/11/2021.10.27-Letter-to-NIH.pdf

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with divergent S proteins, confirming the value of this model in assessing novel SARS related coronavirus pathogenicity." (Emphasis added).[117]

Despite running two years behind in submitting required reports to NIH, and the failure of EcoHealth to stop the experiments and report to NIAID as promised, NIH approved the renewal of EcoHealth's grant on June 18, 2018. In its November 5, 2018, progress report to NIH for the period of June 1, 2014, through May 31 2019, EcoHealth reported that the strains of viruses it was using could represent a significant threat to public health because they could escape existing vaccine and therapeutic treatments.[118]

The Congressional letter raises many important issues that need to be investigated and ends with a long list of demands from the NIH concerning the agency's grants to, and management and oversight of EcoHealth Alliance.

[117] IBID
[118] IBID

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From the Declaration by Andrew Huff Ph.D.,
Former Employee of EcoHealth Alliance

After being promoted to Vice President of EcoHealth Alliance, Dr. Huff had access to information about the organization's finances. He learned that EcoHealth was heavily dependent on government contracts to remain solvent and that cash flow was often tight. He also observed first-hand that EcoHealth engaged in minor fraud by overbilling time on contracts and double-dipping on some contracts between government agencies and provide donors.

Dr. Huff was routinely involved in meetings and informal discussions during which gain-of-function research was discussed.

During direct participation in the USAID PREDICT program, Dr. Huff saw first-hand that EcoHealth failed to pay adequate attention to biosafety, biosecurity, and risk management. The organization did not perform proper oversight of foreign laboratories at which research funded by EcoHealth took place. Dr. Huff expressed his concerns regularly and they were routinely dismissed by Daszak and other EcoHealth staff.

Dr. Huff met Dr. Shi Zhengli and Dr. Ralph Baric and attended presentations at which they discussed their work on the design and engineering of SARS-CoV-2 and the use of humanized mice in their experiments.

Dr. Huff was involved in the creation of a slide deck presented to In-Q-Tel which included the use of USAID PREDICT funding to collect coronavirus samples from bats all over the world, to analyze these viruses to identify their most dangerous features to humans, and then create chimeras to test on humanized mice.

Other Individuals, Research Institutions, and Organizations of Interest

The Rockefeller Foundation has given several grants to EcoHealth Alliance for the purpose of forming a network called One Health Alliance in South Asia (OHASA) for the purpose of investigating emerging infectious diseases, including bat viruses that have the potential to spread to humans.[119] [120]

In 2010, the Rockefeller Foundation published a report in partnership with the Global Business Network titled "Scenarios for the Future of Technology and International Development."[121] The collaboration used "scenario planning" to look at possible responses to hypothetical situations, including a pandemic. A scenario titled "LOCK STEP" describes a world of tighter top-down government control and more authoritarian leadership with innovation and growing citizen pushback after a pandemic is declared. The events described in this report are eerily like what started taking place in 2020.

In September 2020, The Rockefeller Foundation published a "Message Handbook" for "COVID-19 Testing and Tracing." The Handbook was designed to teach health professionals and others how "…to motivate the public to participate in testing and tracing." The Handbook provides messages developed through research, expert interviews, and testing that have been shown to lower resistance to regular testing and contact tracing. Readers are encouraged to reinforce "new norms" that include "ongoing, repetitive actions." These include:

> "Doctors, nurses, and health care workers are putting their lives at risk to care for people who need it. They need our help. Contact tracing stops more people from getting sick, so hospitals don't get crowded, doctors and nurses can stay safe, and every patient gets the attention they need."

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[119] The Rockefeller Initiative. Disease Surveillance Networks. https://www.rockefellerfoundation.org/wp-content/uploads/Disease-Surveillance-Networks-Initiative.pdf

[120] Epstein JH, Quan PL, Briese T et al. "Identification of GBV-D, a Novel GB-like Flavivirus From Old World Frugivorous Bats (*Pteropus gigantus*) in Bangladesh." *PLoS* 2010 Jul https://doi.org/10.1371/journal.ppat.1000972

[121] Technology's Power to Transform the Lives of the Poor Revealed in New Study by the Rockefeller Foundation and Monitor's Global Business Network."
https://www.tmcnet.com/usubmit/2010/06/21/4859175.htm#google_vignette accessed 9.10.2022

> "If you test positive, there is a short window of time to pinpoint who else might have the virus before they could lose their health and their jobs. If you identify who you were in contact with, you can stop the virus in its tracks."[122]

In August 2022, https://www.rockefellerfoundation.org/news/mercury-project-to-boost-covid-19-vaccination-rates-and-counter-public-health-mis-and-disinformation-in-17-countries-worldwide/

UC Davis One Health Institute leads the PREDICT Project, with partners including EcoHealth Alliance, Metabiota, and the Smithsonian Institute. The purpose of this project is to "…enable global surveillance for pathogens that can spillover from animal hosts to people…" and "…discover viruses of pandemic potential."[123]

In a series of emails between members of the PREDICT research team obtained by US Right To Know:

EcoHealth Alliance made requests via the predict-outbreak@ucdavis.edu email system for travel approval for Dr. Peng Zhou and Dr. Shi Zhengli to travel to the U.S. Both were listed as "PREDICT China Country Coordinators," both were listed as working at the Wuhan Institute of Virology, and both were traveling to the U.S. to meet with the PREDICT global team at EcoHealth Alliance for "China project updates."[124]

Metabiota also made several similar requests for foreign researchers to visit the U.S.

Emails also discuss subgrants through EcoHealth to other countries including China; and funds to Metabiota with subawards to other countries.

Many emails pertain to the Global Virome Project, which involves Nathan Wolfe at Metabiota and endeavors to "…identify virtually every viral pathogen on the planet."

Some emails refer to PREDICT work in Laos, which is one of the sources of bat viruses which were sent to The Wuhan Institute, one of which has a genetic sequence almost identical to SARS-CoV-2 (discussed in this manuscript above).

One journal article included in the document with the emails describes a PREDICT project that involved isolation of an Ebola virus from bats in Sierra Leone.

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[122] Rockefeller Foundation. Message Handbook: COVID-19 Testing and Tracing. September 2020
[123] https://whc.vetmed.ucdavis.edu/predict-project accessed 9.10.2022
[124] https://usrtk.org/wp-content/uploads/2021/10/UC-Davis-Jonna-Mazet-batch-1.pdf accessed 9.10.2022

Many names in the email exchanges are redacted.[125]

METABIOTA is an EcoHealth Alliance and UC Davis partner and received investment from the CIA and DoD investment firm In-Q-Tel[126] and numerous contracts and/or grants from the US government. Metabiota was funded in part by Rosemont Seneca, partially owned by Hunter Biden. An In-Q-Tel quarterly report titled “Mission Possible: Quenching Epidemics” lists Metabiota and EcoHealth Alliance as partners.[127]

Metabiota was also part of a consortium that included EcoHealth Alliance, University of California Davis and others. This group was formed as part of the second phase of USAID PREDICT program to investigate coronaviruses, influenza viruses, and filoviruses such as Ebola.[128] EcoHealth’s Fiscal Year Annual report 2014 report confirms this arrangement.[129]

University of North Carolina Chapel Hill, Ralph Baric
Here are just a few of the projects involving Ralph Baric and conducted at or in partnership with UNCH:

Baric, in partnership with Chinese researchers, isolated and studied coronaviruses from bats with HKU spike protein. Funded by National Institutes of Health Grant R01AI89728 and R21AI109094
Yang Y, Du L, Liu C et al. “Receptor usage and cell entry of bat coronavirus HKU4 provide insight into bat-to-human transmission of MERS coronavirus.” *PNAS* 2014;Aug;111(34):12516-12521

Baric and Shi Zhengli collaborated to study the virus surface spikes of MERS-CoV and a related bat coronavirus HKU4. Although HKU4 could not mediate viral entry into human cells, two mutations allowed it to do so.
Yang Y, Liu C, Du L et al. “Two Mutations Were Critical for Bat-to-Human Transmission of Middle East Respiratory Syndrome Coronavirus.” *J Virol* 2015 Sep;89(17):9119-9123
Funded by NIH Grants R01AI089728 and R01AI110700

[125] https://usrtk.org/wp-content/uploads/2021/10/UC-Davis-Jonna-Mazet-batch-1.pdf accessed 9.10.2022
[126] John T. Reinert. In-Q-Tel: The Central intelligence Agency as Venture Capitalist. https://scholarlycommons.law.northwestern.edu/njilb/vol33/iss3/4/ accessed 9.10.2022
[127] IQT Quarterly. Mission Possible: Quenching Epidemics. Winter 2016;7(3)
[128] USAID Announced Second Phase of Predict Project with Global Partners. November 21 2014. https://www.ecohealthalliance.org/2014/11/usaid-announces-second-phase-of-predict-project-with-global-partners accessed 9.10.2022
[129] EcoHealth Alliance Fiscal Year 2014 Annual Report. https://www.ecohealthalliance.org/wp-content/uploads/2016/01/EcoHealth_Alliance_FY14_Annual_Report.pdf accessed 9.10.2022

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Baric and Shi Zhengli were both part of the research team which generated a chimeric SARS-CoV virus that could infect humans. Symptoms in infected humanized mice were similar to symptoms of SARS-C-V-2
Menachery VD, Yount BL, Debbink K et al. "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence." *Nat Med* 2015 Nov;21:1508-1513
Funded by grants from NIH and NIAID: U19AI109761 (R.S.B.), U19AI107810 (R.S.B.), AI085524 (W.A.M.), F32AI102561 (V.D.M.) and K99AG049092 (V.D.M.), USAID-EPT-PREDICT funding from EcoHealth Alliance

Columbia University
The Department of Ecology, Evolution and Environmental and Environmental Biology lists three individuals with EcoHealth Alliance, including Peter Daszak, as faculty members.[130]

Columbia University Mailman School of Public Health announced a partnership with several organizations, including EcoHealth, to launch and operate New York City's first Pandemic Response Institute. The website states that this "…builds on Columbia's robust involvement in the NYC COVID-19 response and grants it a significant role in preparing New York City for future public health emergencies."[131] EcoHealth's website lists Columbia University as a partner.[132]

Yunnan Institute of Endemic Disease Control and Prevention
Received funding from The National Institute of Allergy and Infectious Disease (Grant #R01AI110964). Peter Daszak and EcoHealth served as consultants.
Li H, Daszak F, Chmura A, Zhang Y, Terry P, Fielder M. "Knowledge, Attitude and Practice Regarding Zoonotic Risk in Wildlife Trade, Southern China." *EcoHealth* 2021 Mar;18(2):95-106

Guandlong Provincial Center for Disease Control and Prevention
Daszak authored papers with researchers from this institution concerning pathogens with pandemic potential. Funding was provided by "…generous support of the American people through the United States Agency for International Development (USAID) Emerging Pandemic Threats PREDICT program (Cooperative Agreement No. AID-OAA-A-14-00102)."
Monagin C, Paccha B. Liang N et al. "Serologic and behavioral risk survey of workers with wildlife contact in China." *PLoS One* 2018 Apr;13(4):e0194647

Wellcome Trust

[130] https://e3b.columbia.edu/faculty_location/eha-eco-health-alliance/ accessed 9.10.2022
[131] https://neighbors.columbia.edu/news/columbia-university-mailman-school-public-health-lead-new-york-citys-pandemic-response accessed 9.10.2022
[132] https://www.ecohealthalliance.org/partners accessed 9.10.2022

Has a data sharing agreement with many organizations in public health emergencies. These include EcoHealth Alliance, The Chinese Academy of Sciences, and [133]The Chinese Centre for Disease Control and Prevention.

Google
Google.org has been funding studies conducted by EcoHealth Alliance since 2010.
Here are some of the studies that include Daszak and/or EcoHealth Alliance Vice President Jonathon Epstein as authors and list Google as a funder:

Epstein JH, Quan PL, Briese T et al. "Identification of GBV-D, a Novel GB-like Flavivirus from Old World Frugiverous Bats (*Pteropus giganteus)* in Bangladesh." *PLoS Pathog* 2010 Jul;6(7):e1000972

Pernet O, Schneider BS, Beaty SM et al. "Evidence for henipavirus spillover into human populations in Africa." *Nature Comm* 2014 Sep;5:5342

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The Wuhan Institute of Virology
The University of North Carolina at Chapel Hill
For reasons stated earlier in this paper

[133] https://wellcome.org/press-release/statement-data-sharing-public-health-emergencies accessed 9.10.2022

Declaration of Dr. Andrew G. Huff, PhD, M.S.

I attest that the following is a true and accurate representation of facts and my experiences:

Name: Andrew G. Huff, PhD, M.S.

Personal History/Background/Qualifications:

- From 2002 to 2008 I served in the U.S. Army in both the Minnesota National Guard and on active duty in the US Army as an infantryman.

- I was ordered to serve on active duty to support and fight in the Global War on Terrorism as part Operation Enduring Freedom as an infantryman in Central America, and I volunteered to serve in combat in Operation Iraqi Freedom, where I received numerous medals, awards, and accolades at the low ranks of Private First Class and Specialist.

- While performing combat operations in Iraq, I continued my undergraduate studies while it was my turn to sleep and prepared and competed in Non-Commissioned Officer Review Boards, where I performed the best among the candidates in all aspects of the review except fitness. I was also nominated by my commanding officer to attend Officer Candidate School at the end of my tour in Iraq, based on my performance, leadership ability, and success at executing officer level tasks, which were assigned to me.

- After returning home from Iraq, I completed a heavily research and quantitatively focused bachelor's degree in Psychology at the University of Minnesota, which is one of the top psychological research institutions in the world. I worked directly with many of the world's leading experts in personality, vocational, career interests, clinical, and counseling psychology research, and completed independent quantitative psychological research which was submitted for peer review publication.

- Simultaneously, to earning my Bachelor's degree, I was a program assistant and contracts technical representative (COTR) for the United States Department of Veterans Affairs, where I relocated and opened several new outpatient mental healthcare offices for the agency and managed numerous contracts and relationships with healthcare providers. My supervisor became severely ill, and I independently and successfully managed the organization and contract facilities across the upper Midwest and staff in his absence at the age of 26, which resulted in a financial bonus paid by the government.

- Next, I earned a master's degree in Security Technologies with a minor in Geographic Information Systems, finishing at the top of my class, from the College of Science and Engineering at the University of Minnesota. In the program, I learned to solve national security problems against different types of critical infrastructures using complex systems analysis, systems modeling, high performance computing, intelligence collection techniques and trade craft, international security, bioterrorism, behavioral threat analysis, cryptography, cyber security, vulnerability, and risk assessment among other things. Upon completion of my master's degree coursework and research thesis defense, in only fifteen months, my thesis committee strongly encouraged me to obtain a PhD and was informed that I should meet with one of my instructors which was a member of the faculty in the School of Public Health.

- After meeting with Dr. Jeff Bender from the School of Public Health and College of Veterinary Medicine at the University of Minnesota, I was offered full employment as a Research Fellow at a Department of Homeland Security Center of Excellence at the University of Minnesota, along with a full scholarship to obtain a Ph.D. related to the fields of bioterrorism, biowarfare, chemical warfare or terrorism, pandemics, and emerging infectious disease. This is the best possible offer a Ph.D. student can receive anywhere throughout academia and is rare.

- I earned a Ph.D. from the University of Minnesota's School of Public Health's Environmental Health Science program with a specialization in Emerging Infectious Diseases. My core focus of my education and research was pandemic preparedness response, bioterrorism, biowarfare, biosecurity, chemical attacks & exposures, and biosafety. I completed the program at a record pace (around 3 years) and all my novel research was published in peer reviewed and referred journals before I submitted my dissertation for review.

- While working as a Research Fellow at a Department of Homeland Security Center of Excellence, I frequently traveled to Washington, D.C. and around the country where I became in an active member of US government committees and meetings related to pandemics, public health, and national security. I was introduced to many high-level managers within the US government working in these areas, and I frequently presented my research at US government meetings, to executives in the private sector at large multinational companies, and worked directly with industry and state governments to help improve their national security in areas where I have subject matter expertise.

- Upon completing my Ph.D., I was recruited by Sandia National Laboratories, where I served the U.S. Government as a Senior Member of the Technical Staff and held a Department of Energy 'Q' clearance (equivalent to the Department of Defense's Top-

Secret designation). At Sandia, I analyzed complex national security problems in my areas of expertise, served as a subject matter expert in public health systems and food systems, and participated in a broad spectrum of projects related to pandemic preparedness, mitigation, and response. Wishing to leave the classified work environment, and due to a funding shortfall in my area of passion (preventing intentional contamination of the food supply), I decided to seek work elsewhere in the fall of 2014 and I applied to EcoHealth Alliance in September of 2014.

- Shortly after applying to a position at EcoHealth Alliance, I interviewed with Dr. Peter Daszak on the telephone and then traveled to EcoHealth Alliance's office in New York City for a comprehensive on-site interview. After completing the interview, I was offered and accepted a position as a Senior Scientist in charge of the Data and Technology team. Upon beginning work at EcoHealth Alliance, I was asked to perform a series of duties which would be considered normal in any kind of scientific or academic organization.

Information Related to EcoHealth Alliance and the Development of SARS-COV2:

- In late 2014, I was asked to prepare a report for the Intelligence Advanced Research Projects Activity, Office of the Directorate of National Intelligence, (IARPA). I later learned upon promotion to Associate Vice President while attending weekly finance updates that EcoHealth Alliance did not receive any funding from this agency (IARPA), as far as I am aware. **Reference: IARPA Collaborator Report from Dr. Huff's documents retained from his employment at EcoHealth Alliance.**

- In late 2014, I was asked to review (provide edits, comments, and feedback) on a research proposal that was in preparation to be submitted to the National Institutes of Health's (NIH) National Institute for Allergens and Infectious Diseases (NIAID) to conduct Gain of Function research and development with numerous partners including the Wuhan Institute of Virology, which was supported by Dr. Ralph Baric at the University of North Carolina (UNC). **Reference: File name "CoV as submitted" titles "Understanding the Risk of Bat Coronavirus Emergence" Dr. Huff's documents retained from his employment at EcoHealth Alliance.**

    - I attest that I reviewed the proposal that was submitted to NIH which detailed the gain of function virology work that was being conducted to create the agent known as SARS-COV2, which causes the disease known as COVID-19.

    - I attest that the proposal clearly stated that the gain of function work on SARS-COV2 was already underway in China, prior to October 2014, at the Wuhan

Institute of Virology (WIV), with the support of USAID in collaboration with EcoHealth Alliance and EcoHealth Alliance's partners and sponsors.

- I attest that I made Dr. Peter Daszak aware of the lack of a Biological Security Officer (BSO) and Institutional Biosafety Committee (IBC) at EcoHealth Alliance in reference to the Select Agent Form on in the "Understanding the risk of Bat Coronavirus Emergence" proposal in accordance NIH requirements.

- I witnessed firsthand presentations by Dr. Shi Zhengli (WIV) and Dr. Ralph Baric (UNC) at EcoHealth Alliance related to their Gain of Function work managed and supported by EcoHealth Alliance.

- I witnessed firsthand presentations by the executive team at EcoHealth Alliance related to the gain of function work conducted at EcoHealth Alliance.

- I attest that EcoHealth Alliance~~'s~~ developed SARS-COV2 and is responsible for the development of the agent SARS-COV2 during my employment at the organization.

- I attest that I informed the EcoHealth Alliance executive team that I believed there were biosafety and biosecurity risks in contract laboratories during an executive meeting. Specifically, I was concerned that EcoHealth Alliance did not have enough visibility or firsthand knowledge of what was happening at foreign laboratories contracted and managed by EcoHealth Alliance. During this meeting I discussed bio-risk management with the team due to these concerns. Dr. Daszak refused to mitigate the risks without any objection or discussion from the other executives. In my opinion, Daszak was dismissive of my concerns. He did not seem concerned about EcoHealth's lack of oversight which I felt was strange because it is typically the CEO's duty to protect the organization from organizational threats and risks. After raising my concern, I accepted Peter's position that our control measures were adequate. **Reference: See leaked cables that the US Consulate Cables to the State Department reported Laboratory Safety Concerns at the Wuhan Institute of Virology.**

- In this same short time-period, I was asked to review and contribute to an investment "pitch dick" (i.e., a PowerPoint presentation used in venture capital presentations) that was presented to an organization called In-Q-Tel. In the pitch dick, we proposed an extension of the USAID global disease surveillance work, SARS-COV2 gain of function and humanized mice research conducted by Drs. Baric and Zhengli, and my work from my department developing advanced biosurveillance technologies and platforms. This

work was presented to In-Q-Tel (which can be verified by their own records). I do not know what the outcome of that meeting as it was not communicated to me by Dr. Daszak. **Reference: File name Peter Daszak In-Q-Tel October 2015 from Dr. Huff's documents retained from his employment at EcoHealth Alliance and the In-Q-Tel Quarterly report.**

- On or around June 2015, I was promoted to Vice President. After being promoted to Vice President, I was exposed and participated in more aspects of the organization, as would be expected from an Executive Officer at any organization.

- I began attending weekly financial meetings where I learned that the organization was tight on cash, depended heavily on government contract salary overhead to remain solvent, and that the organization was not involved in traditional conservation work as classically defined. This was upsetting as this was one of the main reasons that I wanted to join the organization (being a conservationist and naturalist). **Reference: EcoHealth Alliance Marketing video from Dr. Huff's documents retained from his employment at EcoHealth Alliance.**

- I also observed that EcoHealth Alliance was engaged in irregular financial transactions regarding U.S. Government grants. Specifically, I believe there was timecard fraud and observed what I appear to be double dipping on contracts, between government organizations and private donors (e.g., Skoll Foundation, Google Foundation, Bill & Melinda Gates Foundation, & Wellcome Trust), or both. **Reference: Compare stated objectives, work locations, and data collection across a range of projects from Dr. Huff's documents retained from his employment at EcoHealth Alliance.**

- I later confronted Dr. Peter Daszak, Harvey Kasdan (CFO, deceased), Dr. Aleksei Chmura about the financial fraud when I was upset, arguing for pay raises in my department, company-wide salary increases, and for myself. Shortly thereafter (1-2 days), CFO Harvey Kasdan passed away from a heart attack. I am not insinuating foul play, but I believe the stress was too much for him in his physical condition. ***R*eference: Harvey Kasdan's Obituary.**

- I also observed, while attending board meetings and in communications directly with board members, that Dr. Peter Daszak had a pattern of over-simplifying and lying by omission to our stakeholders (including the board of directors). For example, while EcoHealth Alliance positioned itself as a conservation organization, no substantial conservation work, as traditionally defined, was occurring at the organization.

- The USAID Predict program was a global hunt for viruses predicated upon the promise of predicting and preventing pandemics. I believe that the data limitations and methods for collecting and analyzing that data make this goal impossible to achieve. I further believe that this program is more strongly aligned with collecting the biological samples to conduct gain of function viral work, or intelligence collection, than prediction and prevention of pandemics.

- Gain of function research is a highly contentious topic in my scientific area of expertise. Those who are for it make the argument that if you can identify a high-risk pathogen, and then engineer the pathogen in the laboratory to increase its transmissibility, infectivity, pathogenicity, or virulence, then you can develop medical countermeasures to prevent the spread of disease, if an outbreak of a **naturally evolving** agent were to occur. I believe this logic to be inherently flawed because **it is naïve to think that humans can modify or engineer a naturally occurring pathogen that would evolve similar to the way infectious agents naturally evolve.** Typically, Gain of Function research (via selection of rare traits or genetic manipulation or engineering of the agent) undergoes **thousands of years of *unnatural evolution* (decided by humans not by nature) in a laboratory in a matter of days weeks or months.** This is akin to predicting the future, with the likelihood of success decreasing in every timestep.

- After being promoted to Vice President, I commented on several concerns I had related to protecting the organization including biosafety, biosecurity, enterprise security, and risk management. None of the other executives voiced any opposition to Gain of Function research being conducted at EcoHealth Alliance, and Dr. Daszak was heavily supportive of the work. Drs. Johnathan Epstein and Kevin Olival were supportive of the work and were key contributors to the gain of function work in the SARS-COV2 proposal funded by USAID and NIH, and executed by EcoHealth Alliance, the WIV, and UNC. My opposition to Gain of Functions research stemmed from my Ph.D. studies taught by my Committee Chair, Dr. Michael T. Osterholm, who was also President Joe Biden's COVID advisor.

- In November 2015, a scientifically peer reviewed, and referenced article was published by collaborators from the Wuhan Institute of Virology, the University of North Carolina Chapel Hill (UNC), the Food and Drug Administration, Harvard Medical School, and the Bellinzona Institute of Microbiology. The peer reviewed article was titled "A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence" in the journal *Nature Medicine.* The authors initially omitted the funding source from the USAID - EPT - PREDICT program, which I was a co-investigator and country coordinator while employed by EcoHealth Alliance. The USAID - EPT - PREDICT funding cited in the article was used to develop a relationship between Drs. Ralph Baric

(UNC) and Zhengli-Li Shi of the Wuhan Institute of Virology at EcoHealth Alliance, which was orchestrated by Dr. Peter Daszak. Additionally, the USAID- EPT - PREDICT funding used in this peer reviewed paper was used to collect biological samples from bats globally. Then, the collaborators analyzed the collected samples to extract SARS like-corona viruses, and select or engineer genetic features within the viruses, collected with USAID - EPT - PREDICT funding, to create hybrid chimeric viruses. Chimeric viruses are defined as combining the genetic material from two or more distinct viruses. **The process of developing SARS-COV2 was also described in detail in the proposal submitted to, and ultimately funded by, the National Institutes of Health (HHS NIH), The National Institute of Allergy and Infectious Diseases (NIAID), by EcoHealth Alliance with the WIV and UNC listed as collaborators.** It is my attestation, that the creation of these SARS-like chimeric viruses described in this article include SARS-COV2. Lastly, the engineered SARS-COV2 was then used to test SARS vaccines and monoclonal antibody therapeutics against the disease in mice. **Reference: Menachery, V. D., Yount, B. L., Debbink, K., Agnihothram, S., Gralinski, L. E., Plante, J. A., ... & Baric, R. S. (2015). A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence.** ***Nature medicine*****,** ***21*****(12), 1508-1513.**

- Dr. Peter Daszak approached me in late 2015 and stated that somebody from the Central Intelligence Agency (CIA) approached him and stated that they were interested in the places we were working, the people we were working with, and the data we were collecting. Peter then proceeded to ask me for my advice, and specifically asked whether we should work with them. I was shocked that Peter asked me this and was excited for the opportunity. I stated to Peter that “It never hurts to talk to them. There could be money in it.” Peter then later confirmed over the next 2 months, between our weekly meetings that the relationship with them was proceeding.

- In March 2016, a paper was published by Dr. Ralph Baric, an EcoHealth Alliance gain of function collaborator working at UNC, in PNAS titled “SARS-like WIV1-CoV Poised for Human Emergence.” In the article, the authors of the paper describe in detail how they used, designed, and constructed full-length and chimeric viruses to determine if they would replicate in human airway cultures. This specific paper is relevant because it compares and documents the effectiveness of different variations of coronavirus spike proteins at infecting human cells specifically by binding to ACE2 receptor, which was a critical and necessary step to design and engineer the SARS-COV2 virus. While employed at EcoHealth Alliance, I met both Dr. Shi Zhengli and Dr. Ralph Baric, where they presented their work on the design and engineering of SARS-CoV2 (coronavirus

gain of function research), and the use of highly specialized humanized mice models, which were necessary to successfully build SARS-COV2. These facts are supported by numerous recorded presentations by Dr. Peter Daszak and Dr. Ralph Baric from 2015-2019. Some of which, I personally attended while employed at EcoHealth Alliance. Additionally, the specific gain of function work described in this paper was presented by Dr. Peter Daszak to In-Q-Tel, a DoD and CIA venture capital firm. In the slides presented to In-Q-Tel, which I personally helped create at EcoHealth, describe the use of USAID – EPT – PREDICT funding to collect coronavirus samples from bats globally, where they are then analyzed to identify their most dangerous features to humans, and recombined to make new coronaviruses like SARS-COV2. Then, these viruses are tested on humanized mice to validate lethality and transmissibility. EcoHealth Alliance then used Dr. Baric's work for testing experimental vaccines, treatments, and therapeutics against the newly engineered SARS-COV2 strain to determine which countermeasures would be the most effective at mitigating the disease in humanized mice. **Reference: Menachery, V. D., Yount Jr, B. L., Sims, A. C., Debbink, K., Agnihothram, S. S., Gralinski, L. E., ... & Baric, R. S. (2016). SARS-like WIV1-CoV poised for human emergence. *Proceedings of the National Academy of Sciences*, *113*(11), 3048-3053.**

- In late September or early October of 2019, I was contacted by Dr. Amy Jenkins and she was attempting to recruit me to be a Program Manager for emerging infectious disease work at the Defense Advanced Research Projects Agency (DARPA). I first met Dr. Amy Jenkins as a Ph.D. student and paid Research Fellow at a Department of Homeland Security Center of Excellence at the University of Minnesota in 2014. The position at DARPA was presented to me as if it was mine if I wanted it and I was told that it would need Top Secret Security clearance with a polygraph. I felt that the recruitment effort was quite strange as I had not worked full-time and directly in the national security space since 2014 at Sandia National Laboratories and I had no clue how Dr. Jenkins obtained my new personal cell phone number. Coincidentally, this is when epidemiological evidence indicates that the first cases of COVID-19 likely emerged. The two events may not be related; however, it is my belief that people working within the US government potentially identified me as a risk to knowing firsthand that the SARS-COV2 disease emergence event was a consequence of the US government's sponsorship of the genetic engineering of SARS-COV2 domestically and abroad. If I would have accepted the position, then I suspect that DARPA would have disclosed restricted information to me which would have consequently prevented me from discussing any of this information publicly, like I have been and am doing now. The recruitment effort itself was highly suspect as it seemed as if DARPA was completely circumventing the US government recruitment process for one of the most prestigious scientific positions in the world.

- I attest that I analyzed the funding of Dr. Kristian Andersen of the Scripps Research Institute from data obtained from NIH funding databases. Dr. Andersen's funding dramatically increased after changing his position on the characterization of the agent as being manmade, to naturally emerging, after a series of discussions with Dr. Anthony Fauci.

Total Funding Awarded Per Month Before Fauci Teleconference	**Total Funding Awarded Per Month After Fauci Teleconference**
$393,079.65	**$800,139.15**
Total Funding Awarded Per Calendar Year Before Fauci Teleconference	**Total Funding Awarded Per Calendar Year After Fauci Teleconference**
$ 1,042,628.25	**$2,284,161.08**
Total Continuing Funding Before Fauci Teleconference	**Total Continuing Funding After Fauci Teleconference**
$7,141,011.83	**$23,724,681.83**

Total Continuing Funding INCREASE After Fauci Teleconference

$16,583,670.00

- Lastly, at no point in time has any restricted information, including classified information, been shared with me related to the domestic or foreign engineering of the biological agent SARS-COV2, the subsequent release of SARS-COV2, the attempted cover-up of by officials working for the United States government. I have never leaked any legally obtained classified information or violated the rules and laws related to my past security clearances. The information that I have shared from my time at EcoHealth Alliance is not restricted by any non-disclosure agreement, nor is it US government protected or restricted information, as EcoHealth Alliance is supposedly a non-profit

corporation conducting scientific research to protect human and animal health. All the documents that I have shared were created by myself or other personnel by EcoHealth Alliance and were not subject to derivative classification by the US government, which is standard practice in academic institutions. My findings, opinions, and analysis were informed by my highly specialized education in the field of emerging infectious diseases from one of the top 5 graduate programs in the world, by my experience working in the field, and by analysis of publicly available open source and open access information. Simply, I know how and where to find accurate and relevant information related to pandemics, emerging diseases, biowarfare, and bioterrorism quickly and know how to properly frame this information from my knowledge of how the government works in the context of relevant policy frameworks.

- In context, this series of events when they took place, did not seem of any consequence nor did I ever think or believe that I would be in this terrible position. I have been severely harassed by what appears to be state-sponsored actors based on the level of sophistication, persistence, and duration, of the harassment and crimes committed against me. I understand that these facts are difficult for our country. I have viewed this as a non-partisan issue since coming forward as a Whistleblower, as my only goal is to prevent another manmade pandemic from occurring. COVID-19, the disease caused by SARS COV2, in my professional opinion, is the result of Gain of Function research that was mismanaged by EcoHealth Alliance and its contractors.

I declare (or certify, verify, or state) under penalty of perjury under the laws of the United States of America that the foregoing is true and correct.

Executed On (Date): 13 September 2022

Signature: [signature]
Andrew G. Huff, Ph.D., M.S.